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TITLE Disease resistance factors JOURNAL Patent: WO 068406-A 21 [1-0.02, 2000], FRATURES E.I. DU POND REMOURS AND COMPANY (US) FRATURES I. Location/Qualifiers 1. Location/Qualifiers A.D. Location/Qualifiers A.D. Score 2288; DB 6; Length 2288; A.D. Exef="taxon:3847"	CTTCC CGTGC CGTGC CGTGC CGTGC CAAGG CAAGG CAAGG

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Submitted (01-DEC-1997) School of Biological Sciences, University of East Anglia, University Plain, Norwich, Norfolk NR4 7TJ, England Location/Qualifiers
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 2291)
Feys,B.J., Benedetti,C.S., Penfold,C.N. and Turner,J.G.
Arabidopsis mutants selected for resistance to the phytotoxin
coronatine are male sterile, insensitive to methyl jasmonate, and
Fessers I to 2291)
Pethogen
2 (bases 1 to 2291)
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AY045625 2335 bp mRNA linear PLN 24-JUL-2001 Arabidopsis thaliana At2g39940/T28M21.10 mRNA, complete cds. AY045625 AY045525.1 GI:15010647 FLI_CDNA.

RESULT 3 AY045625 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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Xipunitation

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/t-anslation="WedPDIKEK48CVATVDDVIEQVMTYITDPKDRDSASLVCREW

FKIDSETREHVTWALCYTATPDRLSRRFPNLRSLKLKGKFRAAMFNLIPENWGGYVTF

WYPEISNLKADLKSCSTRFRADDLETLALDKCSGFTTGGLLSIV

THCRKIKTLARESS FSEKGGKWALRILAQRMYSLEVLMFYMTBFAKISPKDLSIV

CRSLVSVKVGDFEILELVGFFKAAANLEBFCGGSLNEDIGMPEKYMNLVFFRKLCRLG
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ESLESIGTVLKNLCDFRLVLDREBERTTDLPLDNGVRSLLIGCKKLRRFAFYLRQGGL
TDLGLSYTGQYSPWYRMLLGYVGESDEGLMBFSRGCPNLQKLEMRGCCFSBERIARA
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this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
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                                                                                                               Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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|mol_type="mRNRA"
|db_xref="taxon:3702"
|chromosome="2"
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1779)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L.,
Carninci, P., Chang, E., Dale, J. M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jones, T., Kanin, A., Karlin-Neumann, G., Kawai, J.,
Ishida, J., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., AY133556 1779 bp mRNA linear PLN Arabidopsis thaliana At2g39940/T28M21.10 mRNA, complete AX133556

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347 708 407 828

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ISMOPNEMPTLEPFRAQIRKLDLIYALLETBHCTLIQVCRNLEVLETRNVIGDRGL
EVLAQYCKQLKRL RERGADRGMEDREGLVSQRGIJALAQCQCGETSVAAVYSDITN
ESLESIGTYLKNLCDPRLVLLDREERITDLPLDNGVRSILIGCKKLRRFAFYLRQGG
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VTKLPSLRYLWVQGYRASMTGQDLMQMARPYWNIELIPSRRVPEVNQQGEIREMEHPA
HILAYYSLAGQRTDCPTTVRVLKEPI"
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FYRIDSTREATHYWALCYTATPDRISREPPINESLEXLKKKRFAÄNFUNLEPBWGGYVTP
WYTEISNNLRQLKSVHFRRMYVSDLDLDRLAKRRADDLETLKLDKCKSGFTTDGLILSIY
HYCRKIKTLLMEBSSFBSKDGKMLHELAQHINTSLEVLNPYMTEPAKISPKDLETIARN
                                                                                                                                                                                                                                                   Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L.,
Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K.,
and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAS: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L., Chan, M.M., Chang, R., Dale, J.M., Deng, J.M., Goldsmitch, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Theologis, A., and Ecker, J.R.
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Suthwick,R., Tang,C.C., Toriumi,M., Mu,H.C., Yamada,K., Yamgamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collection and clustering of RAFL CDNAS (RAFL CDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-701-2002) Salk Institute Genomic Analysis Laboratory
(SIGTAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
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/note="This clone is in pUNI 51"
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/product="At2g39940/T28M21.10"
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db_xref="GI:22137082"
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'db_xref="taxon:3702"
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Best Local Similarity 67.8%;
Matches 1160; Conservative
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VCRRWHRIDALTRKHVVARFCYAARPARLAERFPPRLESISLKGKPRAAMYGLIPDDWG
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptouphyta; Embryophyta; Tracheophyta;
Spermarcophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaa.
I (basea I to 2088)
Wang,W. and Wang,X.
Direct Submission
Submicted (12-0-7-2002) Biochemistry, Fudan University, 220 Handan Road, Shanghai 200433, P.R. China
Location/Qualifiers
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                       AAGCATAGGCACATÁTCTGAAAACCTCTGTGACTTCCGCCTTGTCTTACTCGACGGGA
                                                                 CAAGCTGAGGAGATTTGCTCTATATCTCAGGCGTGGCGGGTTGACTGATGTAGGCCTTGG
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ACATATTGGAACTCACTTGAAGAACCTCTGTGATTTTCGCCTTGTGTTGCTTGACCATGA
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AY168645.1 GI:37359392
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/db_xref="taxon:39947"
/chromosome="1"
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FLGLTYMGTNEMPVI FPFSMKLKKLDLQYTFLTTEDHCQI IAKCPNLLILEVRNVIGD
RGLEWVGDTCKKLRRLRI BRGDDDPGLQEGGSVGGLTAVNSVGREBELST IAAVYSD
ITNGALBSIGTFCKNLYDPRLVLLDRERQYTDLLDNGVCALLRNCTKLRFALYTRA
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SLAVLQMPSLRYIWVQGYRASQTGLDLLLMARPFWNIEFTPPSPESFNHMTEDGEBCV
DSHAQVLAYYSLAGRSGCPWVIPLHPA" 1004 1118 4 1064 GITTAACATATATGGAAAGAATGAGTTGCCCATTGTGTTCATGTTTGCAGCCGTACTAA 1178 720 780 840 900 483 764 543 824 884 663 944 404 243 524 584 363 644 423 704 603 183 464 303 aegcecirceaccirceccecareaccercaccacceccaccacarcecceccerrareace ACCGCGGTCACGTGCTTCACGCTCTCAAGCTTGACAAGTGCTCCGGTTTCACCACCGATG AGACTCTCAATTTTTACTTGACAGACATTGCTGTTGTGAAGATTGAGGACCTTGAACTTT 664 reacacreaacrircracareacreacrica ---caaacreeccaccacrearcracacrirc trocadagadirocancatrontricarrodadagarodagionoganicadatic TIGIGAACTICITIAAGCAIGCCICIGGGCIGGAAGAGITITIGIGGAGGCACCIACAACG rgarragritritricaaacagccaargcgcrigcaagacritrgcriggaggagcarrcracg AGGAACCAGA-----AAGATACTCTGCTATATCATTACCAGCAAAGTTATGTCGATTGG 484 cécecesacacarecrecases es construitos de construitor de constr CAATICTIGAGAAGGACGGAGAATGGCTACACGAGCTTGCTTTGAATAATACAGTTCTTG AGAGCCTCCACTTCCGCCGCATGATTGTCAAGGATTCCGATCTTCAGAATCTCGCTGTG 604 ATATTACTGATAAGGGTGGTGAATGGCTTCATGAACTTGCTGTCAACAATTCTGTTCTGG dacirececcicacida de caracida de caracida de caracida de decidades de caracidades TOGAGTOGOTOAAGCTCAAGGGCAAGCCCCCGAAGCTGTTCAACTTGATACCCGAGG rcasgrescrerescressasses de asecces de contrar de contrar de contrar de contrar de contrar de contrar de contra de contrar <u> Acricedececeracionecente arteancea ca acrece con contra acrece con contra a contra</u> GTGTGGTCGACGTGCTCGACTGCGTCATCCCTTACATCGACGACCCCCAAGGACCGCG ACCCCGTTTCCCCACGTGTGTCCACGCTGGTACGAGCTCGACTCGCTCACCCCCAAGCACG TCACCATCGCGCTCTGCTACACCACCACCGGCTCGCCTCCGCCGCCGCTTCCCGCACC ATTGGGGCGGACACGTCACTCCCTGGGTCAAAGAGATTTCTCAGTACTTCGATTGCCTCA Gaps 15; Length 2088; IndelB Score 685.8; DB 8; Pred. No. 3.6e-151; 0; Mismatches 617; Query Match
Best Local Similarity 63.7%;
Matches 1111; Conservative

1238

(atFBL2)

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                                                                                                                   Unpublished
2 (bases to 711)
Christiansen, L.C. and Ulvskov, P.
Christiansen, L.C. and Ulvskov, P.
Direct Submission
Submitted (08-AUG-2002) Biotechnology Group, Danish Institute of Submitted (08-AUG-2002) Florechnology Group, Danish Institute of Languary Sciences, Thorvaldsensvej 40, Frederiksberg C 1871,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to Arabidopsis COI1 (atFBL2)
                                                                   1 (bases 1 to 711)
Christiansen,L.C. and Ulvskov,P.
Putative Glycine max sbCOII homologous to Arabidopsis COI
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                                                                                                                                                                                                                                                 /organism="Glycine max"
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                                                                                                                                                                                                                    Location/Qualifiers
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/gene="COI1"
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TICE: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagaahira,N., Doi,K., Khishimato,N., Yamada,H., Oka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,N. and Nakahama,Y.
Ful Genome Sequencing k. Analysis Group: Otomo,Y., Iida,Y.,
Ful Genome Sequencing k. Analysis Group: Otomo,Y., Iida,Y.,
Ryu,R., Sugano,S., Yokama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Kie,Q., Yokomizo,S., Yokhimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Science Laboratory in Riken: Adachi,J., Alzawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Haraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katch,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matuyama,T., Miyazaki,A., Murata,M.,
Ota,Y., Sattoh,H., Saaki,C., Sakai,K.,
Sakarune,N., Sano,H., Saaski,D., Sato,K., Shibata,K.,
Tagami,A., And Hayashizaki,Y.
Tagami-Takeda,Y., Tagawa,H., Toya,T., Waki,K.,
Takaki-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M.,
Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Tanaka, T., Tomaru, A., Toya, T., Tennoda, Y., Ueda, M., Waki, K.,
Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J.,
Yokomizo, S. and Yoshimura, A.
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ive 0; Mismatches 615; Indels 15; Gaps
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033032A10"
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Oryza sativa (japonica cultivar-group) cDNA clone:J033032AlO, full
insert sequence.
AK121543
                                                                                                                                                                                                                                                             1923 AGTTGATTCCTTCTAGAAAGGTGGCTACGAATACCAATCCAATGAGACTGTAGTTGTTG 1982
                                                                                                                 1863 ATGGTGTATCTCCATCTGGACGTGATCTTTTGGTAATGGCTCGACCCTTTTGGAACATTG 1922
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                               554 AGTTGATTCCTTCTAGAAAGGTGGCTACGAATACCAATCCAGATGAGACTGTAGTTGTTG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 AGCATCCTGCTCATATTCTTGCATATTATTCTCTTGCAGGGCAGAGATCAGATTTTCCAG 673
           494 AIGGIGIAICICCAICIGGACGIGAICITITIGGIAAIGGCICGACCITITIGGAACAITG
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9. SINGLE CONTROLLES C	1607 GGACAGTACAGTGGAATTATCCAATACATGGTTCTGGGTAATT 1727 GGGCTTTTGGAGTTGCTAAGGGGTGTCTTGGGTAAA 1667 GGTCTGATCGGTTGCTAGGGGTGTCTTCTGGGAAG 1737 TTATTTTCAGTGAACGTGCATTGGGGTGTGGAACCTGGGGAAG 1724 TGTGGTTCAGTGAACGTTAGGCTGTGGCTGCAAGAGTTAGGCTGGTTAGGCTGAAGGTTAAGGCTGTTAGGCTGAAGGTTAAGGCTGTTAGGCTGAAGGTTAAGGCTGTTAGGCTGAAGGTTAAGGCTGAAGGTTAAGAGTTAAGAGTTAAGAGTTAAGAGAGTTAAGAGAGTTAAGAAG	AKIO1514 Oryza sativa (japonica cultivar-group) CDNA insert sequence. AKIO1514 AKIO1514 AKIO1514 AKIO1514 AKIO1514 GI:32986723 FLI CDNA; CAP trapper. Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embr Spermatrophyta; Magnoliophyta; Lilopsida; Pospermatrophyta; Namida; Pospermatrophyta; Satoh, K., Namiki, T., Ohneda, E., Yahagi, W., Ohtsuki, K., Shighiki, T., Poundation of Advan Science Genome Sequencing & Analysis Group; Ilda, Y., Sugano, S., Fujimura, T., Suzuki, Y., Kuroshi, T., Manna, T.,	Natikawa, N. Josayamari, T. Tatan, N. Yoshimuz Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsud Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsud Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsud, K., Hara, A., Hashidume, W., Hayatsu, N., Inotani, N. Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Salto, R., Sahati, N., Sabati, N., Sato, K., Shibata, R., Si Saito, R., Sanda, J., Sato, K., Shibata, R., Si Soience and Hayashizaki, Y. Collection, mapping, and annotation of over japonica rice soin (5631), 376-379 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 22752273 (2003) 2275273 (2003) 22752273 (2003) 2275227 (2003) 2275227 (2003) 2275227 (2003) 227527 (2003
6.99 GARCACTOACTCCCTGGGTCANAGAGITTCTCAGACTTCTCTAGAGGCTCTCGGGGCCCCCCCCCC		5 L 5 56	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS
	GGACACGTCACTCCTGGGTCAAAGAGTTTCTCAGTACTTCGATTGCCTCAAGAGCCTC	TTCTTTAAGCATGCCTCTGCGGAAGAGTTTTGTGGAGGCACCTACAACGAGGAACCA TTTTCCGGATGGCTGCAACATTGCGGGGGGCACTTCATTGAGGAAGG TTTTCCGGATGGCTGCTATATCATTACCAGGAAGGGCATTCATT	GAGGATGAAGAAGGTACTGTGTCCCAIAGAGGGCTAATAGCCTTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCACAGGGCTGTCTGT

tional Institute of

cDNA Project Team:
hira, N., Dol.,K.,
mada,H., Ooka,H., Hotta,I.,
W., Suzuki,K., Li,C.,
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up:, Otomo,Y., Murakami,K.,
Y., Tsunoda,Y.,
ashi,M., Xie,Q., Lu,M.,
comizo,S., Nikura,J.,
ciminx,A., Miura,J.,
tsubara,K., RIKEN:
'K., Arakawa,T., Fukuda,S.,
in,K., Arakawa,T., Fukuda,S.,
in,K., Ishii,Y., Itoh,M.,
shinagawa,A., Shiraki,T., 'a, A., Carninci, P., Doi, K.,
'a, A., Hashizume, W.,
'Hiramoto, K., Hiraoka, T.,
'da, R., Imamura, K.,
'awa, M., Itoh, M., Kagawa, I.,
'awa, I., Kawamata, M.,
'awai, J., Kawamata, M.,
'awai, J., Kobayashi, M.,
'i., Konno, H., Kouda, M., r 28,000 cDNA clones from CATATTATTCTTTGCAGGG 2023 linear PLN 24-JUL-2003 A clone:J033046F05, full |||| |||||| \argingggaaacagaigai 1666 |||||| |GCTTGA---GCTAAGGAGT 1723 ATTGACTTCTTTAGGTAC 1846 TACGAATACCAATCCAGAT 1966 ACTTGAAATGAGAGGTGT 1786 ATCITITGGIAATGGCICGA 1906 bryophyta; Tracheophyta; Poales; Poaceae; CTGC 2067

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GGAACTCACTTGAAGAACCTCTGTGATTTTCGCCTTGTGTTGCTTGACCATGAAGAGAAG 1546
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Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayasu, M., Hiramoto, K., Hiracka, T., Hori, F., Kida, S., Katch, H., Kawai, J., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kooda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Salco, H., Sakai, C., Sakai, K., Sakazume, N., Salo, H., Sasaxi, D., Sato, K., Shibaca, K., Shinagawa, A., Takahashi, F., Takakahi, T., Yawashiza, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yawanishi, A. and Hayashiza, T., Tomaru, A., Toya, T., Waki, K., Yang, Location/Qualifiers
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NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satch, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, V.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.
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Submitted (27-AD02) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
105-6602, Japan (E-mall:skikuchi@nias.affrc.go.jp,
Tel:81-29-888-7007, Fax:81-29-8388-7007, This clone is one of the 28K full-length cDNA clones from japonica
                Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Malzuno,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,M., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami,Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yanamato,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
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/mol type="mRNA"
/cultivar="whipponbare"
/db xref="taxon:39947"
/clone="J033046F05"
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Pred. No. 1.1e-146;
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Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Miura, J., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nakamura, M., Numasaki, R., Ohno, M., Otheuki, K., Oomura, K., Ota, M., Ota, Y., Otono, Y., Ryu, R., Saltoh, H., Sakai, C., Sakai, Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tayawa, T., Tsunoda, Y., Uda, M., Waki, K., Xie, Q., Yahaka, T., Tamanoto, Y., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yeshimura, A.
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rateda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.
Rodama, T., Kursoski, T., Kusumegi, T., Lu, M., Manda, J.,
Mizuno, K., Marikawa, R., Miikura, J., Oka, M., Kyu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,
Ahimura, T., Arakawa, T., Carninoi, P., Fukuda, S., Hanagaki, T.,
Hiraoka, T., Harikawa, T., Carninoi, P., Fukuda, S., Hanagaki, T.,
Hiraoka, T., Horii, F., Idda, J. Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hicozane, T., Kojima, Y., Katoh, H., Kawai, J.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakawa-Hicozane, T., Nomura, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yaunishi, A. and Hayashizaki, Y.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohteuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Indoratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 TCCCAGGIGIGICGACGCTGGIACGAGCTCGACTCGCTCACCAGCAGCACGTCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2300;
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25.4%; Score 581.6; DB 8;
Best Local Similarity 61.1%; Pred. No. 1.7e-126;
Matches 1070; Conservative 0; Mismatches 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nipponbare"
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica sultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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298 GCCATGGCGTACTCCACCACCACCGGCTGTTCAGGCGGTTCCCCTGGCTCGAGTCG 357	CTCAGGTCAAGGGCAAGCCCCGAAGCCGCAATGTTCAACTTGATACCCGAAGATTGGGGGCCCCCAAGCTCCAAGCCCCAAGCCCCGAAGCCCGAAGCCCAAGCCCAAGCCCAAGGCCAAGCCCAAGCCCAAGGACTGAAGCCCAAGGACTGAAGCCCAAGGACAAGCCCAAGGACAAGCCCAAGGACAAGACAAGACAAGACAAGACAAGACAAGACAAGAAG	593 GGACACGTCACTCCTGGGTCAAAGAGTTTCTCAGTACCTTCGATTGCCTCAAGAGCCTC 652	653 CACTTCCGCCGCATGATTGTCAAGGATTCTCGGATCTTCAGAATCTCGGTCGTGACCGCGGGT 712	713 CACGIGCTICACGCTCTCAAGCTIGACAAGTGCTCCGGTTTCACCACGATGGTCTTTTC 772		833 GAGAAGGACGGAGAAITGCTACACGAGCTIGCTITGAAIAAIACAGITCTIGAGACT 889 	890 CTCAATITITACTIGACAGACATIGCIGITGIGAAGATIGAGGCCTIGAACTITIAGCT 949 	AAAAATTGCCCCAACTTAGT CGCAATTGTCGAAGGCTGAA	1010 AACTICTITAAGCATGCCTCTGCGCTGGAAGAGTTTTGTGGAGGCACCTACAACGAGGAA 1069	1070 CCAGAAAGATACTCTGCTATATCATTACCAGCAAAGTTATGTCGA 1114	1115 TIGGITTAACATATATIGGAAAGAATGAGTTGCCCATIGIGITCATGITTGCAGCCGTA 1174	1175 CTAAAAAAATIGGAICTCCTCTAIGCAAIGCTAGACACGGAGGAITGTIGIAIGTIAATC 1234 	1235 CADAGGIGTCCAAATCTGGGAGTCCTTGAGACAAGGAATGTAATTGGAGATAQAGGGTTA 1294 	1295 GAGGITCITGGICGITGITGIAAGAGGCIAAAAAGGCITAGGAITGAAAGGGGGGATGAI 1354 	1355 GATCAAGGAATGGAGGATGAAGGAACTGTGTCCCATAGAGGCTAATAGCCTTG 1411 1195 GATCAAGGAGGTCTTGAGGATGAACATGGTATGGTTACACAGGTGGGGTTGATGGTGATGATAACATGGTAAGGTTGACAGGTGGTGATGATGATGATAACAGGTGGGGTTGATGATGATGATAACAGGTTGATGATGATGATGATGATAACAGGTGGTAA 1254	1412 TCACAGGSCTGTTCAGACTTGAATACATGGSCTGTTTATGTGTCTGATATTACAAATGCA 1471	1472 TCTCTGGAACATATTGGAACTCACTTGAAGAACCTCTGTGATTTTCGCCTTGTGTTTGCTT 1531	1532 GACCATGAAGAGAAGATAACTGATTTGCCACTTGACAATGGGGTCAGGGCTCTACTGAGG 1591
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11-Length cDNA Project Team:
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tion of Advancement of International
lysis Group:, Otomo, Y., Murakami, K.,
Suzuki, Y., Tsunoda, Y., Murakami, K.,
H., Kobayashi, M., Xie, O., Lu, M.,
M., Yokomizo, S., Niikura, J.,
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da, M., Matsubara, K., RIKEN:,
M., Arakawa, T., Pukuda, S.,
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Miyazaki, A., Osato, N., Otay, Y.,
hibata, K., Shinagawa, A., Shiraki, T.,
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S. (bases 1 to 2924)

Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotter, T., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Hayashida, K., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kiuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Koduo, J., Kowamata, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Muura, J., Myazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Iokamura, M.,
Numasaki, T., Marikawa, R., Nikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Sakazume, N., Ota, V., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, C.,
Sakazume, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Yanada, T., Tomaru, A.,
Taya, T., Tsunoda, Y., Wasunitshi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Full Genome Sequencing & Analygis Group: Otomo,Y., Iida,Y., Full Genome Sequencing & Analygis Group: Otomo,Y., Iida,Y., Full Genome Sequencing & Analygis Group: Nobayashi,M., Kodama,T., Kucosaki,T., Kusumegi,T., Lu,M., Masuda,M., Milaa,J., Milara,J., Miran,J., Sugano,S., Sugiyama,A., Suzuki,Y., Mikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Marikabara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Science Center and Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Haraoka,T., Haraoka,T., Hayashirume,W., Hayashi,M., Hayashirume,W., Inda,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitch,H., Sakai,C., Sakai,C., Sakai,C., Sakai,C., Sakaine,N., Sakai, T., Chinarawa, R., Shita, T., C
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Direct Submission

Submission

Submission

Submission

Submission

Agrobiological Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kamnondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,

Tel:81-29-838-7007, Fas.81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
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NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satch, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. a
Yamamoto, M.
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Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGIGGICCICGACIGCGICAICCCITACAICGACGACCCCCAAGGACCGCGACGCCGIT
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61.1%; Pred. No. 1.7e-126;
iive 0; Mismatches 629;
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/cultivar="Nipponbare"
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/clone="J023114118"
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Location/Qualifiers
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/culTivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join(16606. .17390,17822. .18140))
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          COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2078 GGCCTTGGGTACATTGGTGAATTTAGTAAGACAATCCGTTACATGTTACTTGGGAATGTT 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1832 ACTICICITIAGGIACTIGIGGGIGCAAGGITAIGGIGIAICICCAICIGGACGIGAICTI 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2255 AAATCACTGAGATACCTATGGGTGCAAGGATACAAGGCATCTCCCAATGGCACTGATCTA 2314
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Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Busaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (Dases 1 to 108847)
Rounsley, S.D., Retchum, K.A., Lin, X., Phillips, C.A., Brandon, R.C.,
Fuhrmann, J.L., White, O., Kerlavage, A.R., Adams, M.D.,
Somerville, C.R. and Venter, J.C.
                                                                 1898 GCTCTAGAAGCCATCGGTACATACAGCAGCAGTCTTAACGATTTCCGGCTTGTCCTGCTT 1957
                                                                                                                                                                                                                         GGCTGTGACAAGCTGAGGAGATTTGCTCTATATCTCAGGCGTGGCGGGTTGACTGATGTA 1651
                                                                                                                                                                                                                                                                                                                              2138 GGGGAGTCTGACCAAGGACTGCTTCAACTCTCAACAGGATGCCCAAGCTTGCAGAATTG 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1772 GAAATGAGAGGGTGTTTATTTTCAGTGAACGTGCACTTGCTGTGGCTGCAACACAATTG 1831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1892 TIGGIAAIGGCICGACCCTITIGGAACAIIGAGIIGAIICCIICCIAGAAAGGIGGCIACG 1951
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Town, C.D. and Kaul, S.
Direct Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1952 AATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTGTTATTAT
                                                                                                                     GACCATGAAGAGAAGATAACTGATTTGCCACTTGACAATGGGGTGAGGGCTCTACTGAGG
                                                                                                                                                                2018 GGCTGCACCAAGCTCCGGAGGTTCGCATTTTATGTAAGACCTGGGGCTCTATCAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                   1712 GGGGAGICTGATGCAGGGCTTTTGGAGTTCGCTAAGGGGTGTCCTAGTCTTCAGAAACTT
                TCTCTGGAACATATTGGAACTCACTTGAAGAACCTCTGTGATTTTCGCCTTGTGTTTGCTT
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KEYWORDS
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                                                                                                                                                                                                                                                                                 ASLVTFGVLMITLLIALSTMLQSCENRNIAIVEAQRLDESFGYCKILSLHSQLNSLDE
ESELPLLCRDVALHRIKGGIYLRELNFTIQMALTYFQTIKFMNDNCDVVVIDIDDTNL
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                                           .32802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                               translation="MSAYTHPMERELSGLSSRGNSELGSRYSIESGCYMTSLAASIFI
                                                                                                           .32802,
genscan; supported
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>AGCAĞTTGAAGCĞGCTGAĞĞATTGAACGCĞGTĞCAĞATĞAACAAĞGAATĞGAĞĞAĞĞAĞĞ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGTACTGTGTCCCATAGAGGCTAATAGCCTTGTCACAGGGCTGTTCAGAGCTTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42143 ACATGGGGGGGGTGTATGTCTCAGATATAACTAACGAATCTCTTGAAAGCATAGGCACATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAGAAÇÇTÇTGTGATTTTTÇĞÇÇTTĞTĞTTĞĞTTĞACCATĞAAĞAĞAAĞATAACTĞATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTCGCTAAGGGGTGTCCTAGAAACTTGAAATGAGAGGGTGTTTATTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGCTTAĞICTCACAAAGAGATTAATCGCTTTGGCTCAGGGCTGCCAGGAGCTAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12083 IGAAAACCICIGIGACTICCGCCITGICITACTCGACGGGAAGAAAGGATTACAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCACTTGACAATGGGGTGAGGGCTCTACTGAGGGGCTGTGACAAGCTGAGAGATTTG
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                                           .32312,32388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
  T28M21.8; predicted by
           by full length cDNs. Ceres.3701"
complement (join(<31685, .32030,32109.
32903. .33016,33116. .33199))
                                                                                                              join(31862. .32030,32109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%; Score 428; DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g39930"
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630; Conserv
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complement (128872. . 28916)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPNTSSSRIANEESTKSLALACALLASSRSSTHELLSWIPENLSVMGESTFWEISRD
CFSDFSSNSNAEKLVELVEDSEKIEMLPIVLPELKDGIEKSSLGKGSDAEDVSAAMAR
TPVGYAILAAHQLRWFVTQVKKPNLVKFCNLVVPCALTALDHWSPEVKGQGMITFVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein id="AAB95276.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGLICAIFAIGIPHLSALGVWLGVSTFLSLIYIVVAIVLSVRDGVKTPSRDYEIQGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGINSAYVLGYSGTIMVPLGWIGGVVGLLIATAISLYANTLIAKLHEFGGRRHIRYRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: T28M21.6"
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28689. ...28928)
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                                                                                                                                                                   Ceres:39048"
                                                                                                                                                                                                                                                                                                                                                                                                                                  product="
                                                                              /rpt_f
24452.
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OY 1797 GIGAACGIGCACITGCIGTGCAACAATTGACTTCTTAGGIACTTGTGGGIGC 1856		ù	447 TOPTESTON 667
Db 41786 GTGAGCGAGCATCGCTGCGGTTACAAATTGCCTTCACTGAGATACTTGTGGGTAC 41727		i ñ	
OY 1857 AAGGITAIGGIGIATCICCAICIGGACGIGAICITITGGIAAIGGCICGACCCITITGGA 1916	02	9	692 AATCTCGCTCGTG
1917 ACATTACATTACATACAAAQAAAQATACAAAAACAAAAC	名 &	W E	361 AATCTCGCTCGTG 751 TTTCACCACCGAT
Db 41666 ACATCGAGCTGATTCCATCAAGAAGTCCCGGAAGTGAATCAACAAGAGAGAG		4	421 TTTCAACAACGAT
1977 TIGIGAGCALCCIGCICATATICTIGCAGAGAGAGAGATT	λο	ě.	808 GT 809
Db 41606 AGAIGGAGCAICCGGCICAIAIAIIGGCIIACIACICICIGGCIGG	qa	4	481 GT 482
41546 GICCAACAACTGTTAGAGTCCTGAAGGAGCCAATATGATATGACCCAAAAAAGGTT	-	RESULT 14	
2097 TGTGTATATATACCAGTTTTCTTTTGTTTT	LOCUS	LOCUS DEFINITION	AP003279 Oryza sativa (5
	ACCE	ACCESSION	AP003279 BA0000 AP003279.2 GI:
RESULT 13 AXO46779 LOCUS AXO46779 LOCUS AXO46779 DEFINITION Sequence 5 from Patent W00068406. ACCESSION AXO46779		YWOKUS URCE ORGANISM	oryza sativa (j Oryza sativa (j Eukaryota, Viri Spermatophyta;
	REFE	REFERENCE	Ehrhartoldeae;
SOURCE Glycine max (soybean) ORGANISM Glycine max ORGANISM Glycine max Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, robids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae; Glycine	AU AU	THORS	Sagakı, T., Mate Katayose, Y., W. Antonio, B.A., P. Chiden, Y., Haye Hamada, M., Hare Idonuma, A., Ii
REFERENCE 1 AUTHORS Caimi, P.G., Famodu, O.O., Lee, J.M., Miao, G.H. and Maxwell, C.A. TITLE Disease resistance factors JOHNNAL PATENT: WO 0068406-A 5 16-NOV-2000;			Itoh, Y., Itoh, Kikuta, A., Koba Mizuno, H., Mizu Nakama, Y., Naka
a O			Ohta, I., Ono, N. Shomura, A., Sor Yamagata, H., Ya Zhong, H., Iwama
/mol_type="unassigned DNA" /db_xref="taxon:3847" ORIGIN	II O	TITLE JOURNAL	Yano,M., Jiang, The genome mequ Nature 420 (69)
Query Match Best Local Similarity 97.7%; Pred. No. 1.88-86; Matches 471; Conservative 0; Mismatches 5; Indels 6; Gaps 5;		MEDLINE PUBMED REFERENCE AUTHORS	22337376 12447438 2 (bases 1 to Sasaki,T., Mats
Oy 334 GCGGAAGACACGTGGTCGACGTGGTCCTCGACTGCGTCATCCCTTACATCGACGACCC 393 Db 1 GCGGAAGACACGTGTGGTCGACGTGGTCCTCGACTGCGTCATCCTTACATCGACGACCC 60	06	JOURNAL	Submitted (19-1 Agrobiological 2-1-2, Tsukuba
Qy 394 CAAGACCGCGACGCGTTTCCCAGGTGTCGACGCTGGTACGAGCTCGACTCGCTCAC 453 Db 61 CAAGGACCGCGTTTCCCAGGTGTCGACGCTGGTACGAGCTCGACTCGTCAC 120	COMMENT	ENT	Tel:81-298-38-' On Sep 20, 2007 Genes were pre-
Qy 454 CCGCAAGCACGTCACCACCTGCTACACCACCCCGGGCTCGCCTCGCCGCCG 513 Db 121 CCGCAAGCACGTCACACCACCACCACCACCACCACCGCGCCGCGCGCG			(October 1998 'NCBI NonRedund: (ftp://ncbi.nl)
OY 514 CTTCCCGCACCTCGAGTCGCTCAAGGTCAAGGCCAAGCCCCGAGCCGCAATGTTCAACTT 573			NCBI NonRedund the identified corresponding 1
Qy 574 GATACCCGAGGATTGGGGCGGACACGTCACTCCCTGGGTCAAGAATTCTC-AGTACT 632 Db 241 GATACCCGAGGATTGGGGGGGACACGTCACTCCCTGGGTCAAAGAGATTTCTCAAGTACT 300			classified basesuch as same na

≵ ક	633 TCGATTGCCTCAAGAGCCTCCACTTCCGCCGCATGATTGTCAA-GGATTCCGATCTTCAG 691
č	692 AATCTCGCTCGTGACCGCGGTCACGTTCACGCTCTC-AAGCTTGACAAGTGCTCCGG 750
qo	61
දු ද	751 TTTCACACACATGGTCTTTCCATATC-GGTCCCTTTTGCAA-GAGTTTAAAGALTT 80/ 421 TTTCAACAACGATGGTCCTTTCCATATCGGGTCGCTTTTGCAAAGAAGTTTAAGAGTCCT 480
à	808 GT 809
qq	481 GT 482
RESULT 14 AP003279 LOCUS DEFINITION ACCESSION VERSION	AP003279 134982 bp N Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:POS2805. AP003279 BA000010 AP003279.2 GI:15718426
KEYWORDS SOURCE ORGANISM	Oryza sativa (japonica cultivar-group) N Oryza sativa (japonica cultivar-group) Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrbartoideae
REFERENCE AUTHORS	Landicoldeac, Organo, Organo, C., Sakata,K., Baba,T., Sagaki,T., Matgumoto,T., Yamamoto,K., Sakata,K., Baba,T., Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y., Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K., Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K., Hamada,M., Harada,C., Hijshita,S., Honda,M., Ichikawa,Y.,
	Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Itoh, S., Itoh, T., Itoh, Y., Mabuchi, A., Machara, T., Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Machara, T., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M., Nakami, Y., Nakamura, M., Namiki, N., Negishi, M., Ohta, I., Ono, N., Sali, S., Sakai, K., Shibata, M., Shimokawa, T., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K., K., Shomura, A., Song, J., Takazaki, Y., Tsuji, K., Waki, K., Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
TITLE	language, i. Imman, i., Ionana, i., Ionana, i., Ionana, I., Iwama, I., Iwama, I., Iwama, I., Iwama, I., Indone, I., Iwama, I., Indone, I., Indone, I., Iwama, I., Indone, I., Indone, I., Iwama, I., Indone, I., I
MEDLIN	22337376 12447438
REFERENCE AUTHORS TITLE	2 (bases 1 to 134982) Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
JOURNAL	Submitted (19-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Ric Genome Research Program; Kannondai
COMMENT	<pre>2-1-2, lBuxkDa, lDatan 303-8000, Datan (E-mail:tBasakl@nias_affrc.go.jp, URb.http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) On Sep 20, 2001 this sequence version replaced gi:13027309.</pre>
	Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NORT Nonredundant Protein database. In
	(ftp://ncbi.nlm.nlh.gov/blast/db) and the cDNA sequence database at (ftp://ncbi.nlm.nlh.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.
	A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering

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WERFEFFRE LEDUE LIBEAL FV VILBAIDE LIFE VORTED FOR VILL SCHELE FOR VARENCE AND MICHAED FROM VILL SCHELE FOR VARENCE AND WITH SCHELE FOR VARENCE AND WITH SCHELE FOR VARIABLE AND WITH SEASOPKEP PYDLIKES FWYDARS Y VERY LAY VILL SCHER FRENCHER STANDER PRESENGENE FOR SCHER FOR SCHER FOR SCHER FROM SCHED FOR THE VERSIGN SPECIAL PRESENGE FOR SCHERE FOR YOUNGS SARRER BETWIE FROM SCHERE FOR 
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42150. .42599)}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALAAAAAAAAGTARADEPQRRSCDVRGHSTIWSLFHQDDRGRVPSSSSAADIAPPHQ
QPPPPPRPFIPDDFLDEDIPVVMEHDEIMPVVEPVIVVDTSGEIETEPNVVAREGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(23661. .23843,23923. .24021,24116. .24189,
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                                                                                       complement (join(14141. .14355,14614. .14942,15117. .15432,
15672. .15826,15966. .16014,16692. .18537))
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                                                                                                                                                                                 complement (join(14141. .14355,14614. .14942,15117. .15432,
15672. .15826,15966. .16014,16692. .18537))
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                                                                                                                                                                                                                                                                            /gene="P0529E05.5"
/note="hypothetical protein"
/codon start=1
/protein_id="BAB84390.1"
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/gene="P0529E05.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (30042. .34424)
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                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="GI:18461193"
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RRPIERGRGRHQRLTTQWALRKCRDGDAVVAMDARMRRTSAVVAAMEKVWALAAECTA
PDRAARPAMRRCAEVLWSIRRDPGQRAATAAAAARGKRHDGSTYGESITYGESITSLKE"
complement (join (7920 . #104, #190 . #223, #332 . #469,
#893 . 9039,9136 . 9180,9283 . 9646,9758 . 9984,10424 . 10843))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(7920. .8104,8190. .8223,8332. .8469,
8893. .9039,9136. .9180,9283. .9646,9758. .9984,10424. .10843))
/gene="PO529805.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MARPEGGLIPLARSLIPLSAPPFVSGRRRRLPTLVLGRALPPPTW
LPHGRLSPAHPLPFAPPRRISRPPPPATSLPGASPGGGAEAQAVLAEFTSERVTGSRVKVA
LPHGRLSPAHPLPFAPPRRISRPPPPATSLPGASPGGGAEAQAVLAEFTWSTLGGALVDY
MLGLALALCHADRVVMSYATUPLSQRVGTFBERGAVVOSSERVMSYLDSPTIGGALVDY
YGGRVWARYGVALMSLATFLSPWAARSLWHFLSTRVLLGKMEGVALPSMNNWYLRNP
PRTERSSAVGIAMAGROLGKNTTGLLLSPIIMSRAGIFGPFVIFGLFGFLWVLVWISAL
SGTPGBRNAGIGAHTGGGLAKTOGGGGRRIKKVPPFSRLLSKWPPMALISANAM
HSWGYFVILSWMPVYFXIIYHVNLREAAWFSALPWWWAJUGSVAGVVSDELIGNGTS
ITLIRKKIMQTIGFYGGOYALLGIMAAKSPVIAAMITIAVGLKSFGHSGFLVNLQEIA
PQYAGVLHGMSNTAGTFAALLGTVGAGFFVDRMGSFRGFLITTSLLYFSSTLFWDIFA
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complement (join (3596. 3889,3976. 4274,4750. 4839,
5288. 2546,5562. 5684,6335. 6361))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0529805 clone has an overlap with P0239H11 (DDBJ: AP004072) clone at the position 1 to 19,018 of 5' end. The sequence of this clone starts at the position 146,952 of P0529H11. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join(3596. 3889,3976. 4274,4750. 4839,
5288. 5456,5562.
/gene="P0529805.2"
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Oryza sativa (japonica cultivar-group)"
|mol type="genomic DNA"
|cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains EST R03279(R3279)
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/gene="P0529E05.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome="1"
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70103 AGAACCCTGTGTGGATAGCCATGCTCAGGTTCTTGCCTACTATTCCCTTGCTGGAAGGAG 70162
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Evarmyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTTTTGGAGGAAAGCTCAATTCTTGAGAAGG----ACGGAGAATGGCTACACGAGCTTG
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                        TTTGGAGTTCGCTAAGGGGTGTCCTAGTCTTCAGAAACTTGAAATGAGAGGGTGTTTATT
                                                                                                  GATCCGTTTCGCAGTGGGCTGCACCTTCAGAAGCTTGAATTGAGAAGCTG---CTG
                                                                                                                                                                                 TITCAGIGAACGIGCACTIGCTGCCIGCAACACAATIGACTICTCTTAGGTACTIGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTA---GITGITGAGCALCCTGCTCATATTCTTGCATATTATTCTCTTGCAGGGCCAGAG
                                                                                                                                                                                                                                                                                                                                         GGTGCAAGGTTATGGTGTATCTCCATCTGGACGTGATCTTTTGGTAATGGCTCGACCCTT
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Patent: WO 0068406-A. 17 16-NOV-2000;
E.I. DU PONT DE NEMOURS. AND COMPANY (US)
Location/Qualifiers
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                                                                                                                                                        0; Mismatches 467;
                                                                                                                   .7e-78;
/note="hypothetical protein"
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New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
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Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence

Claim 2; Page 59-60; 74pp; English.

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is cDNA from the soybean clone sgs4c.pk003.k23:fis which is homologous to COII. The COII and LISI proteins are involved in disease resistance. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI DNAs of the invention may be used to alter the expression of COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides Sequence 2288 BP; 560 A; 510 C; 546 G; 672 T; 0 U; 0 Other;	Query Match 100.0%; Score 2288; DB 3; Length 2288; Best Local Similarity 100.0%; Pred. No. 0; Matches 2288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GCACGAGGCCACACGTTAC	61 GGGTGTATGTAGCTGTTCCTAGGATGAATATTGTGATAACAGAACGGCGTTTGAAGCAGT 120 	121 GACGIGITACATCAGTACATCACATCACGTAAATATAGGTAATAAGCTGGGAAAA 180 	181 AGITITGICGITICACCCAICTGITIGGCCCIACCAITICCICACICAICACCCCAI 240 181 AGITITGICGITICACACCCAICTGITIGGCCCTACCAITICCICACICAICAICAICACCAI 240	241 AACCCATTCCCCTTTGGCACTTGAACCAAAACCTCTGGACCTTTTTTTT	301 TCTCCGATCCAATATGACGGAGGAACGGAACGGGAAGACACGTGTGGTCGACGTGGT 360	361 CCTCGACTGCGTCATCCCTTACATCGACGACCCCCAAGGACGCGGACGCCGTTTCCCAGGT 420 361 CCTCGACTGCGTCATCCTTACATCGACGACGCGACGCGA	421 GIGICGACGCIGGIACGAGCICGACTCACCCGCAAGCACGICACCAICGCGCICIG 480 421 GIGICGACGCIGGIACGAGCICGACCCCGCAAGCACGICACCAICGCGCICIG 480	481 CTACACCACCCCGGCTCGCCTCCGCCGCTTCCCGCACTCGAGTCGCTCAAGCT 540	541 CAAGGGCAAGCCCGAGCGGAAIGITCAACTIGATACCCGAGGATIGGGGCGGACACGI 600 	601 CACTCCTGGGTCAAAGATTTCTCAGTACTTCGATTGCCTCAAGACCTCCACTTCCG 660	661	721 T	Y 781 TCGCTTTTGCAAGAGTTTAAGAGTCTTGTTTTTGGAGGAAAGCTCAATTCTTGAGAAGGA 840	841 C
88888888 % 8	~ m &	S G	\$ 60 60	95 95	\$ 8	\$ g	8 8	92 da	ζ da	S da	\$ A	දු දු	S da	& A	\$ A	, B Q

or clone sgs4c.pk003.k23:fis which is homologous to proteins are involved in disease resistance. The se invention may be used to alter the expression may be used to alter the expression in calle narrivillarly to produce transcenic	OY 901 CTTGACAGACATTGCTGTTGTGAGGACCTTGAACTTTTAGCTAAAAATTGCCC 960
stemic resistance to a wide range of pathogens. nay be used to identify inhibitors of these seful as herbicides	QY 961 CAACTIAGIGICIGIGAAACTIACIGACIGIGAAAIACIGGAICITGIGAACTITIA 1020
J; 0 Other; Length 2288;	1021 GCATGCCTCTGCG 1021 GCATGCCTCTGCG
); Mismatches 0; Indels 0; Gaps ACAGGGGACTATGGTTGCCGGAACAAATCCGGATGGGAAA	QY 1081 CTCTGCTATATCATTACCAGCAAAGTTATGTCGATTGGGTTTAACATATATTGGAAAGAA 1140
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plants with increased systemic resistance to a wide range of
COII and LLSI proteins may be used to identify inhibitors of
proteins, which may be useful as herbicides
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                                                                                                                                                                                                                                              2100
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An isolated polynucleotide (1) comprising a sequence (Ia) encoding a polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified sequences, given in the specification, or the complements of (Ia), is new Herbicide. (I) encodes disease-resistance factor polypeptides (II) and can be used, in sense or antisense orientation, to alter the expression of (II) in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by (I) are used to raise specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as as described in the method of the invention
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TITCAACAACGAIGGICCITICCAIAICGGGICGCITITIGCAAGAAGAAGTITAAAGAGICCT
                                                     TITCACCACCGAIGGICTIIICCAIAIC-GGICGCTITIGCAA--GAGITIAAGAGICII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens screen for herbicides.
                                                                                                                                                                                                                                                                                                                         cDNA from the soybean clone sg84c.pk003.k23 homologous to COII.
                                                                                                                                                                                                                                                                                                                                                     Corn; rice; soybean; wheat; ATHCOR1; LLS1; disease resistance; A. thaliana coronatine-induced; COI1; herbicide; EST; expressed sequence tag; sgs4c.pk003.k23; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 482 BP; 96 A; 163 C; 118 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product= "COII"
transl except= (pos:305. .308,aa:Xaa)
/note= "Xaa= unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maxwell CA;
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17. .341
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                                                                                                                                                                                                                            AAA95055 standard; cDNA; 482 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2000; 2000WO-US011956.
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Best Local Similarity 97.7°
Matches 471; Conservative
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P-PSDB; AAB23450.
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Gaps

TCTGTGATTTTCGCCTTGTGTTGCTTGACCATGAAGAGAAGATAACTGATTTGCCACTTG

1506

to

and

Claim 2; Page 55; 74pp; English

Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLG1 protein. The present sequence is cDNA from the corn clone p0128.cpici34r:fis which is howologous to COII. The COII and LLG1 proteins are involved in disease resistance. The COII and LLG1 proteins are involved in disease resistance. The COII and LLG1 protein in cells, particialarly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLG1 proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides

Seguence 1728 BP; 496 A; 341 C; 400 G; 491 T; 0 U; 0 Other;

Gaps 27; Score 372.4; DB 3; Length 1728; Pred. No. 6.5e-94; Indels 421; 0; Mismatches 16.3%; 61.0%; 702; Conservative Best Local Similarity Query Match Matches

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TGTTTTTGGAGGAAAGCTCAATTCTTGAGAAGG---ACGGAGAATGGCTACACGAGCT 807

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154 ca----GAGTATCTTACCCTTCTTGTGCGCAACTGTCAACGATTGAAAACTCTGAAGATTA 210 924 AGATTGAGGACCTTGAACTTTTAGCTAAAATTGCCCCCAACTTAGTGTCTGTGAAACTTA

CTGACTGTGAAATACTGGATCTTGTGAACTTCTTTAAGCATGCCTCTGCGCTGGAAGAGT 211 grgangrurcangcccgarcngcrcagrriccaacrgcacaacacacaacaagagr 1044 TTTGTGGAGGCACCTACAACGAGGAACCAGAAAGATACTCTGCTATA-984

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--TCATTACCAGCAAAGTTATGTCGATTTGGGTTTAACATATATTGGAAAGAATGAGTTGC Aciarititccrccrrcaciecaceecrifeaeirifecrciacareeaaacaarearee TCGCTGGTGGTTCCTTTGAAGAGCAGGGTCAACCTGTGGCAAGTAGAAATTATGAGAACT 271 1091

AAATACTGTTTCCATATGCTACTGCACTTAAGAAGTTAGACCTTCAGTTTACATTCCTTT 450 CCATTGTGTTCATGTTTGCAGCCGTACTAAAAAATTGGATCTCCTCTATGCAATGCTAG 1149 391

331

ACACGGAGGATCATTGTATGTTAATCCAAAGGTGTCCCAAATCTGGAAGTCCTTGAGACAA

1209

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510 édgaricircaracidedarcerecaraciterrecacadacerecasadaarrecara 451 CCACAGAGGATCATTGTCAGATAGTTCAACGCTGCTCCAATCTGGAAACCTTAGAGGTGA GGAATGTAATTGGAGATAGAGGGTTAGAGGTTCTTGGTCGTTGTTGTAAGAGGCTAAAAA 1269 511 GGCTTAGGATTGAAAGGGGGGGATGATGATCAAGGA---ATGGAGGATGAAGAAGGTACTG 1385 GECTCAGAGTAGAGAGAGAGATGATCAAGGAGGTCTTGAGGATGAACAAGGTAGGA 571 1329

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TITATGIGICICAGAIATIACAAAIGCAICICIGGAACAIAIIGGAACICACIIGAAGAACC 1505 631 Tricacagenegernearescrarascreaasscriscrereacrisacaracinescen 690 TGTCCCATAGAGGGCTAATAGCCTTGTCACAGGCTGTTCAGAGCTTGAATACATGGCTG 1386

691 Tacardraricadacarracaarrecagorrradagecagrigeracargeagaaaare 750

1865 1167 1625 1745 1047 1107 1685 810 870 990 crrradcirridderidekerachecrraagrekerigaddarerigreddirekaadarrea ACAATGGGGTGAGGGCTCTACTGAGGGCTGTGACAAGCTGAGGAGATTTGCTCTATATC 991 Aadacrideechaderrigeaaaaakergdagaridadagaridrerriri---Adridageard CACTTGCTGTGGCAACACAATTGACTTCTCTTAGGTACTTGTGGGTGCAAGGTTATG GTGTATCTCCATCTGGACGTGATCTTTGGTAATGGCTCGACCCTTTTGGAACATTGAGT traaridacirtoodoctriorcortodradadadadacaararaadaarindocadrod acaarieggeringeringeringagerieggachaachacggagaringcaninare TCAGGCGTGGCGGGTTGACTGGAGGCCTTGGTTACATTGGACAATACAGTCCAAATG ircertaraterrectrestaaretreereaaretearaaresaarearaaraar readaccriatricardiridarcriticaccriatricada and readaccriatricada and readaccriatrical and read TGAGATGGATGCTGCTTGGTTATGTGGGGGAGTCTGATGCAGGGCTTTTGGAGTTCGCTA AGGGGTGTCCTAGTCTTCAGAAACTTGAAATGAGGGGGTGTTTATTTTTCAGTGAACGTG 1168 ATATTGTTCC 1177 1866 1108 1926 1048 1626 871 931 1746 1806 751 811 1686 a g δ g à 셤 ö ద ò 셤 à à g 8

844 standard; cDNA; AAN02372 AAN02372 AAN02372 RESULT

1043

983

1090

270

ВР

rlr2.pk0027.h4, rl0n.pk099.pl4 and rl0n.pk0047.c5 rice; herbicide; disease-resistance factor; (first entry) 당 30-OCT-2001 contig 0011

Oryza sativa.

1148

/transl except= (pos:663. .664,aa:Arg) /note= "This codon has an apparent 1 n which alters the reading frame" .354, aa:Xaa) (poB:352. /partial /transl except= (pos: /note= "Xaa= unknown" Location/Qualifiers 9. .715 'product= "COI1" ø /*tag= Key

nucleotide deletion

WO200068406-A2

L6-NOV-2000

2000WO-US011956 03-MAY-2000;

99US-0133041P 07-MAY-1999;

(DUPO) DU PONT DE NEMOURS & CO E I.

Ğ, Maxwell ษั Miao Lee J, Caimi PG, Famodu OO,

WPI; 2000-687649/67. P-PSDB; AAP01920.

663 GGCCCTTCTGGAACATAGAGTTTACACCTCCCAGAAGACTGGTCACGA

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CC An isolated polymucleotide (I) comprising a sequence (Ia) encoding a colypeptide (II) of at least 60 amino acids (aa) from any of 18 specified CC polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified CC sequences, given in the specification, or the complements of (Ia), is code and isease-resistance factor polypeptides (II) can be used in sense or antiseanse orientation, to alter the expression of (II) in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by (I) are used to raise specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as herbicides. This sequence encodes the rice COII protein created from a contig of rlz2.pk0027.h4, rl0n.pk099.p14 and rlon.pk0047.c5 as described in the method of the invention
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wew nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
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Pred. No. 1e-72;
0; Mismatches 240; Indels
                                                                                                           Claim 2; Page 44; 74pp; English
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65.5%;
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1305 GICGIIGITATAAAAGGCIAAAAAGGCTIAGGATIGAAAGGGCGATGAIGATCAAGGAA 1364
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Pred. No. 1e-72;
0; Mismatches 240;
                                                                                                                         cDNA from a rice contig homologous to COII
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9. .715
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illarity 65.5%;
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                              AAA95054 standard;
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                                                                                                                                                                         Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays List protein. The present sequence is cDNA from the wheat clone wreln.pk0122.d3:fis which is homologous to COII. The COII and LISI proteins are involved in disease resistance. The COII and LISI proteins are involved in disease resistance. The COII and LISI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LISI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
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                                                           New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
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Pred. No. 9e-55;
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                                                                                                                                             Claim 2; Page 66; 74pp; English.
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Best Local Similarity 65.7%;
Matches 356; Conservative
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/product= "COII"
/transl except= (pos:256. .259,aa:Leu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65424-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at sequence.html?DocID=999909770149
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                                                                                                         Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease; stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.
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JP, Haas WD;
Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistance altered metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 161; 40pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         milton CM, Price JL, Raines TM,
Mathew AV, Ledford BL, Woessner
, Slater T, Davis KR, Allen K,
                                                                        Arabidopsis thaliana polynucleotide SEQ ID NO 161
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                                                                                                                                                                                                                                                                                                          26-JAN-2001; 2001US-00770149
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Kricker M,
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
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RAINES T M.
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ALLEN K.
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SLATER T.
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Rameaka JG, Garcia CA,

Hurban P;

Gorlach J,

(HURB/)

(ALLE/) (HOFF/)

DAVI/

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2126

Maxwell CA; Ġ Lee J, Miao WPI; 2000-687649/67. P-PSDB; AAB23451.

Query Match

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                                                                                                                                                       libraries were found to be similar to CDNA encoding the Arabidopsis thaliana COI1 protein and the Zea mays LLS1 protein. The present sequence is cDNA from a wheat contig homologous to COI1. The COI1 and LLS1 proteins are involved in disease resistance. The COI1 and LLS1 DNAs of the invention may be used to alter the expression of COI1 and LLS1 protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLS1 proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
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                                      and
                                                                                                                                      Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA
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.c. .ucretc acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens screen for herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 223.4; DB 3; Length 794; Pred. No. 4.4e-52;
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0; Mismatches 183;
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COII clone contig of wreln.pk0122.d3 and wrln.pk0018.f8.

(first entry)

30-0CT-2001

AAN02374;

AAN02374
ID AAN0
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AC AAN0
XX
DT 30-C
XX
DE COII

ВР

AAN02374 standard; cDNA; 794

RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1576 GAGGGCTCTACTGAGGGGCTGTGACAGCTGAGGAGATTTGCTCTATATCTCAGGCGTGG 1635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polynucleotide (I) comprising a sequence (Ia) encoding a polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified sequences, given in the specification, or the complements of (Ia), is new Herbicide. (I) encodes disease-resistance factor polypeptides (II) and can be used, in sense or antisense orientation, to alter the expression of (II) in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by (I) are used to raise specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as herbicides. This sequence encodes the wheat COII clone created from contigs when the method of intermethod of intermethod of
                                                                                                                /*tag= a
/product= "COII"
/partial
/tansl_except= (pos:253. .256,aa:Asp)
/note= "This codon has an apparent 1 nucleotide insertion
which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AGGATTGATGGCTGTAGCTGAAGGCTGTCCTGATTTGGAGTACTGGGCAGTACATGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1456 TGATATTACAAATGCATCTCTGGAACATATTGGAACTCACTTGAAGAACCTCTGTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reacatracaaarecaecretreagecratregececatreageaaaaccreaaceatrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1396 AGGGCTAATAGCCTTGTCACAGGGCTGTTCAGAGCTTGAATACATGGCTGTTTATGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 cceaciriciccieciridaradadagirecararaacidaacigececiridacaacegegi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 794 BP; 193 A; 165 C; 213 G; 208 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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            COII; wheat; herbicide; disease-resistance factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maxwell
                                                                                                                                                                                                                                                                                                                                                                                                         Miao G,
                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 47; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                         Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%;
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                                                Triticum aestivum
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Seguence 537 BP; 133 A; 98 C; 138 G; 168 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acid molecules (AAH87645-AAH88116) that correspond to all or part of a mRNA molecule expressed in plant oil gland cells, especially peppermint and plant oil glands that produce terpenoid essential oils and resins. The mucleic acids are useful for genetically mapping a plant genome for genes expressed in plant oil gland cells and to suppress (for example by antisense suppression) or enhance their expression (for example by genetically transforming a plant cell with a replicable expression vector that expresses one or more proteins naturally expressed in plant oil gland cells). The nucleic acids are also fiseful for recombinant expression of plant oil gland cells; required for terpenoid essential oil and/or resin production in bacterial and/or yeast cells
                                             1754
                                                                                                        CTAGICITCAGAAACITGAAAIGAGAGGGIGITTATITITTCAGIGAACGIGCACITGCIG 1814
                                                                                                                                                                   TGGCTGCAACACAATTGACTTCTCTTAGGTACTTGTGGGTGCAAGGTTATGGTGTATCTC 1874
                                                                                                                                                                                                                             1875 CATCTGGACGTGATCTTTTGGTAATGGCTCGACCCTTTTGGAACATTGAGTTGATTCCTT 1934
243 AGCTCTATCAGATATTGGCCTTTCTTANGTTGGGCGGAATTTAGCAAGACCGTCCGCTACA 302
                                                                                                                                                                                                                                                  CTACTGGCACCGATCTCATGGCAATGGTACGCCCCTTCTGGAACATTGAGTTTATTGCAC 539
                                                                          rérrecritéggaariecegegegerergarearegaerreceregearitrecaceandariece 362
                                                                                                                                     caadecrigeadaariredadecraadeadrigerecrir---adreaacerecariedead 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules corresponding to mRNA molecules expressed in peppermint oil glands for enhancing expression of plant oil gland cell proteins.
                                             TGCTGCTTGGTTATGTGGGGGAGTCTGATGCAGGGCTTTTGGAGTTCGCTAAGGGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peppermint; plant oil gland cell; terpenoid essential oil; resin; genetic mapping; antisense suppression; recombinant expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peppermint plant oil gland expressed cDNA 117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 122; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wildung
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LANGE B M.
WILDUNG M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488706/53.
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(WILD/)
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                                                                                                                                                                                                                      1764 AGAAACTIGAAAIGAGAGGGIGITIATITITICAGIGAACGIGCACTIGCIGIGGCTGCAA 1823
                                                                                                                                                                                                                                                                                                1824 CACAATTGACTTCTCTTAGGTACTTGTGGGTGCAAGGTTATGGTGTATCTCCATCTGGAC 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                               944 TGGCTACGAATACCAATCCAGATGAGAC----TGTAGTTGTTGAGCATCCTGCTCATATT 1999
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                                                                                                                                                                                                                                                                                                                                  178 Trcacricacccriccaratrificaciacaaccaracricaricarcarcarcarcas
                                                                                                                                                                                                                                                                                                                                                                                                            238 gagarcririnagcaanggccagaccaaarnggaanarcgagringanaccagcracaaggc 297
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                                                                         1 cacaccinescrinscriararacescastacaciaracaaacicacaresarecricic
                                  Gaps
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                                  8
Length 537;
                                    Indels
Score 193.8; DB 5;
Pred. No. 7.9e-44;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peppermint plant oil gland expressed cDNA 229.
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   8.5%;
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                     Best Local Similarity 70.7
Matches 302; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACACT 2065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATCCT 424
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     Query Match
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The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 cadeadececrecaecresinecriceecrateriosaceaecececececececece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1392 BP; 235 A; 441 C; 452 G; 264 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA from the corn clone p0128.cpici34r homologous to COII.
                                                                                                                                                                                                         Goff SA, Moughamer
cke D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 131.6; DB 8 71.4%; Pred. No. 4.7e-26; iive 0; Mismatches 74
                                                                                                                                                                                                         Briggs S, Cooper B, Goff S;
Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1106; 299pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                            22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                       21-JUN-2002; 2002WO-IB002453.
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                                                                                                                                                                                                                               Katagiri F,
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03-JAN-2003
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                                                                          The invention relates to nucleic acid molecules (AAH87645-AAH88116) that correspond to all or part of a mRNA molecule expressed in plant oil gland cells, especially peppermint and plant oil glands that produce terpenoid essential oils and reeins. The nucleic acids are useful for genetically mapping a plant genome for genes expressed in plant oil gland cells and to suppresse (for example by antisense suppression) or enhance their expression (for example by genetically transforming a plant cell with a naturally expressed in plant oil gland cells in naturally expressed in plant oil gland cells). The nucleic acids are also useful for recombinant expression of plant oil gland proteins required for terpenoid essential oil and/or resin production in bacterial and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAACTTGAAATGAGAGGGTGTTTATTTTCAGTGAACGTGCACTTGCTGTGGCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGCTTGAAATGAGAGGGTGT---TGTTTTAGTGAGAGAGCACTAGCTACAGCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 ATATIGITCAIGAIGCAGAAGAGCAACGATTAGIGAICGIIGAAGACCCIGCGCAIAII
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                                                                                                                                                                                                                                                                                                                                                        Sequence 537 BP; 133 A; 98 C; 138 G; 168 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Score 193.8; DB 5; Length
Pred. No. 7.9e-44;
0; Mismatches 117; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease resistance; pathogen tolerance; plant pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conferring disease resistance in plants.
                                       Page 163; 251pp; English
                                                                                                                                                                                                                                                                                                                                                                                               8.5%;
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Best Local Similarity
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Zea mays.

Triticum aestivum.

wheat

WO2003000906-A2

Socation/Qualifiers

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New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides.
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P-PSDB; AAB23448.
                                       WO200068406-A2
                                                                              07-MAY-1999;
                                                    16-NOV-2000
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Lee J, Miao G,

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984 CIGACTGTGAAATACTGGATCTTGTGAACTTCTTTAAGCATGCCTCTGGGCAGAAGT 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1149 CCATTGTGTTCATGTTTGCAGCCGTACTAAAAAATTGGATCTCCTCTATGCAATGCTAG 1208
                                                                                                      Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence is cDNA from the corn clone p0128.cpici34r which is homologous to COII. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI DNAs of the invention may be used to alter the expression of COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.6%; Score 129; DB 3; Length 70 Best Local Similarity 55.5%; Pred. No. 1.7e-25; Matches 318; Conservative 0; Mismatches 234; Indels
Claim 2; Page 42-43; 74pp; English.
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Search completed: April 19, 2004, 18:52:44 Job time : 880 secs

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US-08-232-463-14
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                                                                                                                              (without alignments)
7742.242 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
US-09-232-463-14
US-09-003-287-7
US-09-003-287-7
US-09-029-603-4
US-09-29-004-1
US-09-170-496D-31
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	S DERIVED FROM CORN EAR	132	4 4 4 4	3AACTCACTTGAAGAACCTC 1507
US-09-050-863-2 US-09-359-081-2 US-09-130-114-1 US-09-130-114-1 US-08-47-344A-14 US-08-910-647-1 US-09-620-925-1 US-07-884-811-15 US-07-884-811-15 US-07-884-811-15 US-07-884-811-15 US-07-884-811-15 US-07-884-811-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-088-15 US-08-194-087-15 US-08-194-087-15 US-08-194-087-15 US-08-194-087-15 US-08-194-087-15 US-08-194-087-15 US-08-194-10-158-194-194 US-09-482-273-49	ALIGNMENTS A-1866 66, Application US/09313294A 6476212 **ORMATION: Lalgudi, Raghunath V. Ito, Laura Y. Sherman, Bradley K. Sherman, Bradley K. SNETTION: NUMBER: US/09/313,294A **LING DATE: 1999-05-14 **SEQ ID NOS: 7600 PERL Program **B66 **LING DATE: 1999-05-14 **SEQ ID NOS: 7600 **PERL Program **B66 **LING DATE: 1999-05-14 **REG IN TOOKS: 7600 **REG I	4.6%; Score 105.2; DB 4; Length 266; ; Conservative 0; Mismatches 93; Indels 1; Gaps aggargrantigagaragagggragagggrantggaggggggggggggggg	AGGCTTAGGATTGAAAGGGGCGATGATGATCAAGGAATGGAGGATGAAGAAGGTACTGTG	TAIGTGTCTGATATTACAAATGCATCTCTGGAACATATTGGAACTCACTTGAAGAACCTC
2580 3 2580 3 2580 3 5452 2 5452 2 8705 4 9600 4 10596 1 10596 1 10596 5 16080 4 1151 1 1151 1 1151 1 1151 1 1753 6 6 77536 4	lication US/05 Ni. Mi, Raghunath Laura Y. Nan, Bradley K. Ni. POLYNUCLEP Ni. POLYNUCLEP NI. B. 1999-05-1 TE: 1999-05-1 VOS: 7600 VOS: 7600 VOS: 2000 VOS: 20	4.6% 64.7%, vative ATTGGAGA, ATTGGAGA,	ATTGAAAG ATAGAGCG GGGCTAAT GGCTTGAC	GATATTAC
	294A-1866 1866, Application U. to. 6476212 INFORMATION: NUT: 1LC, Laura Y. NUT: 1LC, Laura Y. NUT: Sherman, Bradle PP INVENTION: PFERENCE: PL-0017 US F APPLICATION NUMBER: F FILING DATE: 1999- 00 SEQ ID NOS: 7600 RE: PERL Program VO 1866 1: 266 10.DNA SEM: Zea mays RE: RES: Misc feature INFORMATION: Incyte 294A-1866	ch 1 Similarity 64. 172; Conservative 68 AGGAATGTAATTGGA 	AGGCTTAGG AGGCTCAGA TCCCATAGA TCTCAAGTG	CATGTGTCT
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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14.4%; Pred. No. 0.0017;
ive 202; Mismatches 216;
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                             Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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(703)683-4109
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLONE: PTZgpt-F18
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OPERATING SYSTEM:
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Best Local Similarity
Matches 71; Conserv
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4%; Score 54; DB 1;
L.6%; Pred. No. 9.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 103)836-9300
                                                                                                                                                                                        Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                            STAIL.
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC compatible
TYPE: PC-DOS/MS_TYPE
            Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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Best Local Similarity 1.6%;
Matches 6; Conservative 2
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                                                                                                    1124 ACATATATTGGAAAGAATGAGTTGCCCATTGTGTTCATGTTTGCAGCCGTACTAAAAAA
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1361 GGAATGGAGGATGAAGAAGTACTGTGTCCCATAGAGGGCTAATAGCCTTGTCACAGGGC 1420
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                                                                      296 CICAGICICCGAICCAAIAIGACGGAGGAACGAACGIGCGGAAGACACGIGIGGGICGAC
                                                                                                                                                                                       CATATTGGAACTCACTTGAAGAACCTCTGTGATTTTTCGCCTTGTGTTGCTTGACCATGAA
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APPLICANT: Jayne, Susan
APPLICANT: Barbour, Eric
APPLICANT: Barbour, Eric
APPLICANT: Meyer, Terry
TITLE OF INVENTION: METHODS FOR IMPROVING TRANSFORMATION BFFICIENCY
FILE REFERENCE: moPAT moCAH
CURRENT APPLICATION NUMBER: US/09/003,287
CURRENT FILING DATE: 1998-01-06
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 735
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48.8%; Pred. No. 0.0028;
tive 0; Mismatches 132; Indels
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Patent No. 6096947
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ORGANISM: Myrothecium verrucaria
FEATURE:
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; LOCATION: (01)..(732)
US-09-003-287-7
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US-09-003-287-7
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Best Local S
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RESULT 5

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Sequence 181, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SSCTWARE: PatentIn version 3.1
SSG IN 0.181
SEQ ID NO 181
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Pred. No. 0.013;
0; Mismatches 147; Indels 0
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APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Dietenhader, Jurg
APPLICANT: Toupet, Christine
APPLICANT: Pospiech, Andreas
APPLICANT: Pospiech, Andreas
FILE REFERENCE: 4-20555/A/PCT
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CURRENT FILING DATE: 1998-03-20
RARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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Patent No. 6210935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.0%;
Best Local Similarity 47.5%;
Matches 133; Conservative
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LOCATION: (378). (1665)
OTHER INFORMATION: ORF
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US-09-170-496D-181
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GENERAL INFORMATION:
-09-170-496D-181
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US-09-029-603-4
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US-09-170-496D-31
US-09-170-496D-31
Sequence 31, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 655539-Endogenous, Constitutively Activated Human G Protein, TITLE OF INVENTION: No. 655639-Endogenous, Constitutively Activated Human G Protein, TITLE OF INVENTION: No. 655639-Endogenous, CONSTENT SEPRENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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                                                                                                              492 coccedenceconcoccecececoccececenceaconcecenceacon
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Pred. No. 0.032;
0; Mismatches 146; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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nes 131; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44.2; DB 3; Length 6 Pred. No. 0.054; 0; Mismatches 128; Indels
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APPLICANT: Tikoo, Suresh
APPLICANT: Tikoo, Suresh
APPLICANT: Babluk, Lozne
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REPERENCE: 293102002400
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTESQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.9%;
Best Local Similarity 48.6%;
Matches 121; Conservative
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LOCATION: (1747) .. (2553)
OTHER INFORMATION: ORF
FEATURE:
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LOCATION: (2593)..(4011)
OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCATION: (5071)..(6085);
OTHER INFORMATION: ORF
US-09-029-603-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587 TGGGGCGGA 595
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Best Local Similarity
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US-09-292-034-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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701..1717
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STATE: Illinois
COUNTRY: USA
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Matches 131; Conserv
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; LOCATION:
US-08-153-848-43
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Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
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    Word Perfect 6.1 for Windows/MS-DOS 6.2
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                                                                                                                                                                                                                                         PA-0002 US
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                              NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
RELECOMMUNICATION INPORMATION:
TELEPAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1484:
SEQUENCE CHARACTERISTICS:
LENGTH: 1900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.3%;
Matches 131; Conservative
                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-016-434-1484
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                                                                                                                                              FILING DATE:
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Sequence 43, Application US/09299843A

Sequence 43, Application US/09299843A

Patent No. 6107475

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun
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OPTWARTING SYSTEM:
OPTWARTING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION NUMBER: US/08/153,848
FILING DATE:
APPLICATION NUMBER: US/08/153,4452
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPRANCATORY INFORMATION:
TELEPRANCATION STATE (312) 474-6300
TELEFRAX: (312) 474-6300
TELEFRAX: 55-386
INFORMATION: (312) 474-6448
TELEFRAX: 55-386
INFORMATION: QUARTICS:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
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PCT-US93-11153-43
; Sequence 43, Application PC/TUS9311153
GENERAL INFORMATION:
, APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.9%;
Best Local Similarity 47.3%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                         STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
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Sequence 43, Application US/09088337B
Patent No. 6348574
GENERAL INPORMATION:
GRAY, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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Pred. No. 0.046;
0; Mismatches 146; Indels 0
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                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27866/32059B FELECOMMUNICATION INFORMATION:
                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299, 843A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UIN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 47.3%;
Matches 131; Conservative (
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(312) 474-0448
                Floppy disk
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EDNESS: single
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                MEDIUM TYPE:
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US-09-088-337B-43
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Pred. No. 0.046;
0; Mismatches 146; Indels 0
STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
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                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 701.1717
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: No. 6748574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHRACTERISTICS:
LENGH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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GOCAYNE,
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; LOCATION:
PCT-US95-07180-1
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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47.3%; Pred. No. 0.046;
iive 0, Mismatches 146; Indels 0;
APPLICANT: Schweikart, Vicki L.
TITLE OP INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1643 AAAAGGCTCAAGGGCCCGCCCCCCAGCTTCGAAGGGA 1679
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORNATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6406
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 47.3
Matches 131; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                90909
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Sequence 1, Application PC/TUS9507180 GENERAL INFORMATION:
APPLICANT: LI, YI

RESULT 14 PCT-US95-07180-1

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1430 Arcancharricricchegericagadacricceccacceccièrecaaciricererese 1489
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                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSES: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSES: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALP: 1,7008
CAMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REGISTRATION NUMBER: 32800-366
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1.744
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APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
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APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
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Patent No. 6114605
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50449 ATTATATTGAĞGATAĞÇĞGTÇTTĞAĞĞAĞATİĞÇÇAAÇAÇTTĞTAAĞGAAÇTTÇAAĞAĞÇ
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APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/947,823 FILING DATE: 09-OCT-1997
                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPRA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 46.5
Matches 264; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                   USA
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April 19, 2004, 20:29:51; Search time 1487 Seconds (without alignments) 6884.896 Million cell updates/sec
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2. (cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

3. (cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*

4. (cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*

5. (cgn2_6/ptodata/2/pubpna/US06 PUBCOMB.seq:*

5. (cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7. (cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8. (cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

10. (cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

11. (cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12. (cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13. (cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

15. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

16. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

17. (cgn2_6/ptodata/2/pubpna/US108_PUBCOMB.seq:*

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19. (cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2288
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 141824,	Sequence 10724, A	Sequence 152, App	Sequence 151, App	Sequence 32228, A	Sequence 8867, Ap	Sequence 33936, A	Sequence 125710,	Sequence 125711,	Sequence 317, App	Sequence 44612, A	Sequence 161, App	Sequence 21331, A
SUMMARIES	US-10-424-599-141824	US-10-425-114-10724	US-10-310-154-152	US-10-310-154-151	US-10-425-114-32228	US-10-425-114-8867	US-10-425-114-33936	US-10-424~599-125710	US-10-424-599-125711	US-10-424-599-317	US-10-424-599-44612	US-09-770-149-161	US-10-424-599-21331
DB	13	13	16	16	13	13	13	13	13	13	13	σ	13
* Query Match Length DB	2305	2011	2178	2419	1503	1325	1469	699	744	829	428	719	449
% Query Match	89.8	86.6	26.7	24.5	17.9	17.6	17.3	14.1	13.6	12.7	12.2	9.9	9.6
Score	2054	1982	609.8	561.2	409.8	403.8	394.8	323	311.6	290.4	279.8	227.2	220.2
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			38104,		Sequence 39506, A		Sequence 97745, A	Sequence 1569, Ap	Sequence 28814, A		34663		Sequence 26663, A	Sequence 1014, Ap	Sequence 287, App	Sequence 93112, A	Seguence 1583, Ap	Sequence 1583, Ap		Sequence 69165, A		34657		Sequence 83717, A	Sequence 45283, A	45	Sequence 1, Appli	493	655	Sequence 137620,
US-10-424-599-21332	US-10-424-599-27395	US-10-424-599-86569	US-10-424-599-38104	US-10-424-599-79984	US-10-424-599-39506	US-10-424-599-32267	US-10-424-599-97745	US-09-294-093B-1569	US-10-424-599-28814	US-10-424-599-5625	US-10-424-599-34663	US-10-424-599-102884	US-10-425-114-26663	US-09-969-373-1014	US-10-310-154-287	US-10-424-599-93112	US-09-923-876-1583	US-09-923-876-1583	US-10-424-599-91753	US-10-424-599-69165	US-10-424-599-130155	US-10-424-599-34657	US-10-424-599-4935	US-10-424-599-83717		US-10-156-761-7456	US-10-156-761-1		US-10-424-599-65547	US-10-424-599-137620
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9.6	8.7	8.5	8.1	7.8	7.3	7.0	5.5	5.4	4.9	4.6	4.6	4.4	4.2	4.2	4.2	3.8	3.6	3.6	3.6	3,3	3.1	3.0	2.9	2.8	2.5	2.3	2.3	2.3	2.5	2.2
218.6	199.2	193.8	185.8	179.6	166.4	160.2	125.4	124.4	112.2	105.8	105.6	99.6	97.2	97	96	86.2	82.8	82.8	81.6	75.6	7.0	68.6	67	65	58.2	52.6	52.6	52.4	51	50.6
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ALIGNMENTS

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Xou Vihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 141824
LENGTH: 2305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 AGACACGTGTGGTCGTGGTCCTCGACTGCGTCATCCCTTACATCGACGACGCCCCAAGG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%; Score 2054; DB 13; Length 2305; 99.5%; Pred. No. 0; Live 0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99079C.1 US-10-424-599-141824
Sequence 141824, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5
Matches 2060; Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Glycine max
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AGCACCOGACCACTACCACATCACTCACCTCACACCCCATACACTCACCCCACA 430 ACCCCCCACCACCACTCCCCCCCCCCCCCCCCCCCCCC	1419 GCTGTTCAGAGCTTGAATACATGGCTGTTTATGGATTTACAAATGGATCTGG 1478

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TICATATIGCTGTTTCTAGTTCCTGCTCTATTTGTAGTTCATTTTAGACAATTAGTCTTG
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    AAAAAATTGGATCTCCTCTATGCAATGCTAGACACGGAGGATCATTGTATGTTAATCCAA
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                                                                                                                                      AAGACACGTGTGGTCGACGTGGTCCTCGACTGCGTCATCCCTTACATCGACGACCCCAAG
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                                                                                                                  AAGCACGTCACCATCGCGCTCTGCTACACCACCCCCGGCTCGCCTCCGCCGCCGCTTC
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                                                                                          1;
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                                                                                          Indels
                                                                            13;
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                                                                           Query Match 87.4%; Score 1999; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 2010; Conservative 0; Mismatches
                                                      ; OTHER INFORMATION: Clone ID: 701002452_FLI
US-10-425-114-11061
2003-04-28
73128
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 11061
LENGTH: 2039
                                        max
                               TYPE: DNA ORGANISM: Glycine FEATURE:
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US-10-425-114-10724
Sequence 10724, Application US/10425114
Sequence 10724, Application No. US20040034888A1
Sequence 10724, Application No. US2004003488BA1
Sequence 10724, Application No. US2004003488BA1
APPLICANT: Expo, Vinua
APPLICANT: ApplicANT: About K.
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER: OF INVENTION NUMBER: 2003-04-28
NUMBER: OF INVENTION NUMBER: 2003-04-28
SEQ ID NO 10724
LENGTH: 2011
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86.6*; Score 1982; I

Best Local Similarity 100.0*; Pred. No. 0;

Matches 1982; Conservative 0; Mismatches
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US-10-425-114-10724
TTAAAAACTGAACATTCTCAATTTTGTGAAT
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                                                                                                                                                                                                                                                                 Length 2178;
                 TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 152
LENGTH: 2178
                                                                                                                                                                                                                                                              26.7%; Score 609.8; DB 16; Length 61.9%; Pred. No. 1.5e-176; ive 0; Mismatches 642; Indels
                                                                                                                                                                                                                                                                                   Best Local Similarity 61.9
Matches 1076; Conservative
                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (130)..(1923)
; OTHER INFORMATION:
US-10-310-154-152
                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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           APPLICANT:
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
McKiel, William G.
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Boddupalli, Raghava
Deikman, Jill
Deng, Molian
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Laccetti, Lucille B.
Lai, Chao-Qiang
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Jung, Vincent
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Hinchey, Brenda S.
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APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 152, Application US/10 Publication No. US20030233670A1 GENERAL INFORMATION:
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, Stephen M.
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Zeng, Xiaoping
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
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Liu, Jingdong
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Sequence 151, Application US/10310154 Publication No. US20030233670A1 GENERAL INFORMATION: APPLICANT: Edgerton, Michael D

RESULT 5 US-10-310-154-151

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387 ACGACCCCAAAGGACCGCGACGCCGTTTCCCCAGGTGTGTCGACGCTGGTACGAGCTCGACT 446
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Pred. No. 1.7e-161;
0; Mismatches 603; Indels 27;
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TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15 (52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 151
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
Start, William G.
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Hinchey, Brenda S.
Huang, Shinbhieh
Johnson, G. Richard
Jung, Vincent
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Laccetti, Lucille B.
Lai, Chao-Qiang
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Deikman, Jill
Deng, Molian
                                                                                                                 Agarwal, Ameeta K.
Ahrens, Jeffrey E.
Ball, James A.
Banu, G.
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Best Local Similarity 61.3%;
Matches 1000; Conservative
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Luethy, Michael M.
Lund, Adrian
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Duff, Stephen M.
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Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
Yang, Chunzhi
Zeng, Xiaoping
Chomet, Paul S.
Adams, Thomas H
                                                                                    Thomas G.
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Zhao, Yajuan
Zhou, Li
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; LOCATION: (139)..(1911)
; OTHER INFORMATION:
US-10-310-154-151
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ORGANISM: Zea mays
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Query Match
Best Local Similarity 60.8%;
Matches 780; Conservative
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ORGANISM: Zea mays
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Sequence 32286, Application US/10425114

Fourierion No. US20040034888A1

Fourierion No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Grown Tone Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: WUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

MUMBER OF SEQ ID NOS: 73128 1866 GIGIAICTICCAICIGGACGIGAICTITIGGIAAIGGCICGACCCTITIGGAACAITGAGI 1925
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j Sequence 8867, Application US/10425114

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j APPLICANT: Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Library Li
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17.6%; Score 403.8; DB 13; Length
Best Local Similarity 60.2%; Pred. No. 4.6e-113;
Matches 726; Conservative 0; Mismatches 467; Indels
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US-10-425-114-8867
ORGANISM: Zea mays
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GGTTATGGTGTATCTCCCATCTGGACGTGATCTTTTGGTAATGGCTCGACCCTTTTGGAAC 1918
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                                                                                                        GIGICIGIGAAACITACIGACIGIGAAATACIGGAICTIGIGAACTICITITAAGCAIGCC 1027
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                                                     GACAITIGCTGTTGTGAAGATTGAGGACCTTGAACTTTTAGCTAAAATTGCCCCAACTTA
  TGGCTACACGAGCTTGCTTTGAATAATACAGTTCTTGAGACTCTCAATTTTTACTTGACA
                       2 IGGCICCAIGAACTCGCIGICAACAATICIGITCIGGGAAAACTGAACTITTACAIGAAC
                                                                                                                                   119 ATTTCTTTGAAGATGGGTGACTGTGATCTTTCAGATCTGATTGGGTTTTTCCAAACCTCC
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Publication No. US20040034888A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack

APPLICANT: Tabaska, Jack

APPLICANT: Tabaska, Jack

APPLICANT: Pants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128

SEQ ID NOS: 73128
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                                                                   Query Match
17.3%; Score 394.8; DB 13; Length 1469;
Best Local Similarity 60.9%; Pred. No. 3e-110;
Matches 753; Conservative 0; Mismatches 462; Indels 21;
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TGTCT 1233
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ORGANISM: Zea mays
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Canou Yihua
APPLICANT: Canou Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 125711
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13.6%; Score 311.6; DB 13; Length
Best Local Similarity 75.1%; Pred. No. 9.1e-85;
Matches 431; Conservative 0; Mismatches 134; Indels
TITGIAGITCATITIAGAÇAATTAGTCITGIAAT 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_84526C.1
US-10-424-599-125711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(744)
OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                            Sequence 125711, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Glycine max
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NAME/KEY: unsure
                                                                                      RESULT 10
US-10-424-599-125711
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 125710
LENGTH: 669
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US-10-424-599-125710
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81.3%; Pred. No. 2.5e-88;
tive 0; Mismatches 86;
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OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                          sequence 125710, Application US/10424599
publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 81.33
Matches 374; Conservative
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US-10-424-599-125710
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323.9)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                  428;
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Pred. No. 4e-75;
0; Mismatches 77; Indels
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US-10-424-599-44612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 161, Application US/09770149 Patent No. US20020059663A1
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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BD.9%;
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Rameaka, Joshua G.
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Kricker, Maja
    Kovalic David K
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Best Local Similarity 80.9
Matches 326; Conservative
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Davis, Keith R.
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                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Glycine max
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                                                                                                                                                                                            SEQ ID NO 44612
LENGTH: 428
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US-09-770-149-161
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APPLICANT:
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APPLICANT: La Rosa Thomas J
APPLICANT: En Rosalic David K
APPLICANT: Rovalic David K
APPLICANT: About Vibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
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12.7%; Score 290.4; DB 13; Length 829;
Best Local Similarity 74.4%; Pred. No. 3.5e-78;
Matches 366; Conservative 0; Mismatches 126; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_100286C.1
US-10-424-599-317
TITIAGITIAGAGGGITICAATITICICIGCAAT 575
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                                                                                                   Sequence 317, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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                                                           RESULT 11
US-10-424-599-317
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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APPLICANT: Zhou Yihua
APPLICANTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-1(53223)8/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 21332
LENGTH: 789
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                                                                                                                                                           Length 449;
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                                                                                                                                                           Score 220.2; DB 13;
Pred. No. 1.1e-56;
0; Mismatches 13;
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                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119267C.1
US-10-424-599-21331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; sequence 21332, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 94.6%;
Matches 228; Conservative
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Best Local Similarity 94.2'
Matches 227; Conservative
LENGTH: 449
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Yihua
APPLICANT: Town Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 21331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1953 ATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTCTTGCATATTATT 2012
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Pred. No. 1.1e-58;
0; Mismatches 173; Indels
                        TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: thaliana FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
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; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 66.7
Matches 356; Conservative
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LENGTH: 719
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307 AGCITGACAAGTGCTTCAGTTTCACCACTGATGGTCTTTTCCACATCGGTCGCTTTTTGCA 366

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Search completed: April 20, 2004, 01:34:07 Job time: 1495 secs

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1 gcacgaggccacacgttaca.....acattctcaattttgtgaat 2288
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	BE821935 GW700015B AY109490 Zea mays AY109565 Zea mays CA820059 sau83h11.
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CA654430 CF807278 DQ133928 BQ133928 B1967384 CF807291 CA820349	A1855554 AW75910 BW75910 BF32527 CB89425 BE80294 BG15655	CB009 CB001 BW894 BW896 BW896 BU80 CB912 CB912 CB912 CB912 CB92 CC996 CC206 CC	BH6789 CB9118 BI8932 CG9455 CG9455 BU5483 BG0443 CA9365 A148298 AW2229
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ALIGNMENTS

FEATURES

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Direct Submission
Submitted (15-APR-2002) Maize Mapping Project, University of Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA corresponding physical clones, these are interested in getting corresponding physical clones, these are publicly available from ZMDB and may be found by BLAST searching at MSL, maizemap.org; ZMDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.nobi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMDB: www.zmdb.iastate.edu.
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1 (bases 1 to 2298)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
                                                                                                                                                                                                                                                                                                                                                    82
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                                                                                                                                        GIGGCIACGAATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTCTT
                                      321 GTGGCTACGAATACCAATCCAGATGAGACTGTAGTTGTTGATGACGTCCTGCTCATATTCTT
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/mol_type="mRNA"
/db_xref="MaizeDB:633078"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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Zea mays CL920_1 mRNA sequence.
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Unpublished (2002)
2 (bases 1 to 2298)
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TITLE
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VERSION
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// Clone='The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from clonal tissues and stages of development of soybean that represent 2,639 sequences from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTS of the source clones from the different library Gm-contig, which were reracked to a representative of each contig, which were reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.

**Reracking was performed by Genome Systems, St. Louis, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Genomics, uniformation on the source library for each clone can also be obstained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."
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Fax: (217) 333-4582
Email: 1-vodkindwiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3322 FXX: (888) 919-3324 or (314)
ystems.com web site:www.genomesystems.com or info@genome
seq primer: 5'-TITITITITITITITITITIT(A/C/G)-3'.
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(Vases I to 2190)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Unpublished (2002)
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Hissouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
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www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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/mol_type="mRNA"
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CA820059 S8 bp mRNA linear EST 09-DEC-2002 Bau83h11.yl Gm-c1048 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1048-2685 5' similar to TR:004197 004197 HYPOTHETICAL PROTEIN.

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XhoI; Wheat (Triticum aestivum L.) root; normalized_from
wrel library"
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                                 AGTTATGTCGATTGGGTTTAACATATTTGGAAAGAATGAGTTGCCCATTGTGTTCATGT
                                                                                              TTGCAGCCGTACTAAAAAATTGGATCTCCTCTATGCAATGCTAGACACGGAGGATCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                        1464 CAPATGCATCTCTGGAACATATTGGAACTCACTTGAAGAACCTCTGTG 1511
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/organism="Triticum aestivum"
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/db_xref="taxon.4565"
/clone="wrein.pk0122.d3:5p5"
/tissue_type="root"
/clone_lib="wrein"
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                                                                                                                                                            1 (bases 1 to 588)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Marra, M., Hiller, L., Khozba, T., Martin, J.,
Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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                                                                                                                                                                                                                                                                                                            Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, M Pax: 314 286 1800
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High quality sequence stop: 421.
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         GGCTGTTCAGAGCTTGAATACATGGCTGTTTATGTGTCTGATATTACAAATGCATCTCTG 1477
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/clone="sHB022K06"
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Tel: 540-231-7318
Email: bmtyler@vt.edu
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Unpublished (2003)
Contact: Tyler B
Tyler lab
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San94ell.y2 Gm-c1054 Glycine max cDNA clone SCYBEAN CLONE ID:
Gm-c1054-2517 5' similar to TR:004197 O04197 HYPOTHETICAL PROTEIN.

N. MRNA sequence.
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/tissue type="mycelium"
/cell_line="p6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="WDBA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2044 TACTGTTGTGCCTTTTGGACACTGCCACATGCGTTGATACCTAGAGGCCAGAGCTGTAT
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23.8%; Score 543.4; DB 14
Best Local Similarity 99.8%; Pred. No. 2.4e-91;
Matches 544; Conservative 0; Mismatches 1;
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Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fmail: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, Ai 35801 For further information.
call: (800)-533-4363 or contact: cou@resgen.com web site:
Www.resgen.com
Seg primer: -408F from Gibco
Seg primer: -408F from Gibco
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                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 420. Location/Qualifiers
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cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University." ORIGIN Query Match Query Match Query Match Query Match Bast Local Similarity 100.0%; Pred. No. 2.4e-90; Ength 538; Marches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	307 ATCCAATATGACGGAAGGAACGGGAAGGAAGACACGTGTGGTCGACGT 1 ATCCAATATGACGGAAGGAACGGAACGTGCGGAAAGACACGTGTGGTCGACGT 367 CTGCGTCATCCTTACATCGACGACCCCAAGGACCCGCGAAGACCCGCGAAGACCCGTGTGCGTTCCCA	61 CTGCGTCATCCCTTACATCGACGCCCAAGGACGCGATTTCCAGGGTCTACCAGGGTCA		SULT 9	B1967384/c B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION B1967384 CERSION CERSION B1967384 CERSION CERSIO	REFERENCE 1 (bases 1 to 561) AUTHORS Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., AUTHORS Vodkin, L., Keim, P., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H. TITLE A Functional Genomics Program for Soybean (NSF 9872565) COMMENT Other_ESTS: AW102154 corresponding to Gm-c1009-1054 (5') Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565) Lewin, H. A., Director, Keck Center for Comparative and Functional
Qy 1837 TCTTAGGTACTTGTGGGTGTATGGTGTATCTCCATCTGGACGTGATCTTTTGGT 1896 Db 361 TCTTAGGTACTTGTGGGTGTATGGTGTATCTCCATCTGGACGTGATCTTTTGGC 420 Qy 1897 AATGGCTGACCTTTTGGACATTGAGTTGATTCCTTCTAGAAGGTGGCTACGAATAC 1956 Db 421 AATGGCTCGCCCCTTTTGGAACATTGAGTTAATTCCTTCTAGAAAGGTGGCTATGAATAC 480 Qy 1957 CAATCCAGATGAGTTGTTGAGTTAATTCCTTCTGCATATTATTCTCT 2016 Db 421 AATGGCTGCAGTTGTTGTTGAGCATCCTGCTCCTTTTTTTT	OY 2017 TGCAGGCCAGAGATTTTCCAGATACTGTT 2050 DD 541 TGCAGGCCAGAGATCAGATTTTCCAGATACTGTT 574 RESULT 8	DEFINITION SET5401-y1 Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1052-3458 5' similar to TR:004197 HYPOTHETICAL PROTEIN. j, mRNA sequence. ACCESSION BQ133928 Glycine max (soybean) ORGANISM Glycine max CNGANISM Glycine max Est. SOURCE Glycine max CNGANISM Glycine max Extractophyta; Embryophyta; Embryophyta; Embryophyta; Expanced on the core endlocets; core endlocets; core endlocets; core endlocets; core endlocets; core endlocets.	RS RS	JOHENAL Unpublished (1999) COMMENT Public Soybean EST Project COMMENT Public Soybean EST Project COMMENT Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: Resden, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:	<pre>www.resgen.com seg primer: -40RP from Gibco</pre>	/clone_lib="Gm-c1052" //note=TWector: pBluescript II SK+; Site_1: BcoRI; Site_2:

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| organism="Phytophthora sojae"

| organism="Phytophthora sojae"

| db xref="texon:67593"

| clone="8HB022P18"

| clisue type="mycelium"

| cisue type="mycelium"

| dev stage="84 hr. post infection stage"

| dav stage="84 hr. post infection stage"

| lab_host="Soybean plant"

| clone lib="USBA-IRFS:Expression of Phytophthora sojae

| clone lib="USBA-IRFS:Expression"

| clone lib="USBA-IRFS:Expression"

| note="Vector: pBK-CMV; Site_1: EcoRl; Site_2: Xhol"
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1951 GAATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTCTTGCATATTA
                                                         261 GAATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTCTTGCATATTA
                                                                                                                                                                                                                          2071 ATGCGTTGATACCTAGAGGCCAGAGCTGTATATATACC-AGTTTTCTTTTGTTTTCT
                                                                                                                                                                                                                                                                           141 ATGCGTTGATACCTAGAGGCCAGAGCTGTGTATATATACCNNNTTTTCTTTTTGTTTTTCT
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Phytophthora sojae
Bukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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Unpublished (2003)
Contact: Tyler B
Tyler lab
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Tel: 540-231-7318
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CF807291/c
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                     Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboration/index
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                                                Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA Tel: (217) 244-6147
Fax: (217) 333-46182
Emai: 1-vodkinduluc.edu
This clone is available through: Incyte Genomics, 4633 World
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Pred. No. 3e-89;
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                                                                                                                                                                                                                                                                                                        Seq primer: 5'-TTTTTTTTTTTTTTT(A/C/G)-3'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                               University of Illinois
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B1974579 538 bp mRNA linear EST 30-NOV-2001 gai70d03.yl Gm-c1068 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1068-3990 5' similar to TR:004197 004197 HYPOTHERICAL PROTEIN: ;, mRNA sequence.
B1974579 I G1:16348984
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Marxa,M., Hiller,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
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                                                           1942
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                                                                                                                                                                                             GCATATTATTCTCTTGCAGGGCAGAGATCAGATTTTCCAGATACTGTTGTGCCTTTGGAC 2062
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                                                                                                                                                                                                                                                                                                                              TTTTTCTTCTCCCCTTTCATATGCTGTTTCTATGTTCCTGCTCTATTTGTAGTTCATTTT
                 ACACAATTGACTTCTCTTAGGTACTGTGTGTGTGTTATGGTGTATCTCCATCTGGA
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                                                                                                                                                           361 Greecraceaaraceaarecaeareaeacreraerieridagearecreereararrerr
                                                                                                                                                                                                              301 GCATATTATTCTCTTGCAGGCAGAGATCAGATTTTCCAGATACTGTTGTGCCTTTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Machington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGCTATTGGCTCCCTTAAAACTGAACATTCTCAATTTTGTGAAT 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGCTATTGCCTCCTTAAAAACTGAACATTCTCAATTTTGTGAAT 16
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/mol_type="mRNA"
                                                             CGIGALCITITGGIAAIGGCICGACCCITI
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//done liber@m.colo68 library was constructed from mRNA isolated from drought atressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were from the into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1068-3990"
/tissue_type="Leaf, drought stressed, 1 month old plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATGTAATTGGAGATAGAGGGTTAGAGGTTCTTGGTCGTTGTTAAGAGGCTAAAA 1327
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                                                                                                greenhouse grown"
/lab host="DH10B"
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Email: est@watBon.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1449 Std Error: 0.00
Seq primer: 40RP from Gibco
High quality sequence stop: 430.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sc20g01.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1013-1225 5' similar to TR:004197 004197 HYPOTHETICAL PROTEIN. 7: mRNA sequence.
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                                                                                                                                                                                                                                                   1952 AATACCAATCCAGATGAGACTGTAGTTGTTGAGCATCCTGCTCATATTCTTGCATATTAT 2011
                                                                                                                                                                                                                                                                                                                                                                         TCTCTTGCAGGGCAGAGATCAGATTTTCCAGATACTGTTGTGCCTTTGGACACTGCCACA 2071
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                                               361 AATACCAATTCAGATGAGACGGTAGTTGTTGTTGAGCATCCTGCTCATATTCTTGCATATTAT 420
                                                                                                                                                                                                                                                                                                                                                                                                            /clone="GENOME SYSTEMS CLONE ID: Gm-c1013-1225"
/tissue_type="whole seedlings, 2-3 week old seedlings,
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Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1800
Fax: 314 286 1810
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/mol_type="mRNA"
/db_xref="taxon:3847"
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/lab host="XL10-Gold"
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South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                         I (bases 1 to 550)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
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/mol type="mRNA"
/db_xref="taxon:3847"
/dlone="SOYBEAN CLONE ID: Gm-c1048-3009".
/tissue_type="whole seedlings of greenhouse grown plants"
//dev stage="1" week old"
/lab_host="0H108"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Ptel: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers
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Arizona University."
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/note="Vector: pBluescript II XR; Site 1: EcoRI, Site 2: XhoI; This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (AT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into Xillo-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
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100.0%; Pred. No. 3.5e-81;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                     Computations (1222)
Contact: Shoemaker R/Public Soybean EST Project
Contact: Shoemaker Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tal: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
This clone is available through: ResGen, Invitrogen Corp. 2130
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1683 AIGIGAAIGGAIGCIGCIIGGIIAIGIGGGGGAGICIGAIGCAGGGCIIIIGGAGIICG 1742
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Schurt, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurt, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1623 ATCTCAGGCGTGGCGGGTTGACTGATGTAGGCCTTGGTTACATTGGACAATACAGTCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch al Similarity 93.3%; Score 476.2; DB 13; Length al Similarity 93.3%; Pred. No. 8.7e-79; 525; Conservative 0; Mismatches 23; Indels
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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 6495 Std Error: 0.00
High quality sequence stop: 422.
Location/Qualifiers
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| Jab host="DH10B" |
| /alb host="DH10B" |
| /clone_lib="Gm-c1027" |
| /note="Vector: PBluescript II SK+; Site_1: EcoRI; Site_2: Sho1; This cDNA library was constructed_from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled with mere propagated on paper towels with distilled
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Mylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Kitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
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                                                                                                              2102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW759107 574 bp mRNA linear EST 03-DEC-2001 sl34g02.yl Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-3243 5' similar to TR:004197 004197 HYPOTHETICAL PROTEIN.
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/db_xref="taxon:3847"
/clone="cBNOME SYSTEMS CLONE ID: Gm-c1027-3243"
/tissue_type="cotyledons of 3- and 7-day-old Williams
                                                                                                                                               2103 TATATACCAGITITCITITGITITICITCCCCTITCARAIGCIGITICIAIGII--CC
                                                                                                                                                                                                                                                                                  366 AGCATCCTGCTCATATTCTTGCTTACTTGCAGGCAGAGATCAGATTTTCCAG
                                                                                                              ATACTGTTGTGCCTTTGGACACTGCCACATGCGTTGATACCTAGAGGCCAGAGCTGTGTA
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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Glycine max
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JOURNAL
COMMENT
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hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAACATAGTCTCGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the CDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the CDNA constructs were size-fractionated with a 500 bp cutoff, using dibocaRI Life Technologies' CDNA Size Fractionation column. The column eluent was then ligated into Stratagene's spluescript (m) II XR Pecalgested vector (pBluescript II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene's 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

ORIGIN

1534 1594 1714 1295 GAGGTTCTTGGTGTTGTTGTAAGAGGCTAAAAAGGCTTAGGATTGAAAGGGGGCGATGAT 1354 GATCAAGGAATGGAGGATGAAGAAGGTACTGTCTCCATAGAGGGCTAATAGCCTTGTCA 1414 CAGGGCTGTTCAGAGCTTGAATACATGGCTGTTTATGTGTCTGATATTACAAATGCATCT 1474 305 1595 TGTGACAAGCTGAAGAATTTGCTCTATATCTCAGGCGTGGCGGGTTGACTGATGTAGGC 1654 1715 GAGTCTGAJGCAGGGCTTTTGGAGTTCGCTAAGGGGGTGTCCTAGTCTTCAGAAACTTGAA 1774 365 424 125 185 245 484 65 66 GAGGIICTIGGICGIIGTIGIAAGAGGCIAAAAAGGCTIAGGAITGAAAGGGGGTGAIGAI 126 garcaaggaarggargaaggargaaggracrgrgrcccaragagggcraarcgccrrgrca 306 CACGAAGAGAAATAACTGATTTGCCACTTGACAATGGGGGTGAGGGCTCTACTGACGGGC 366 idi-acaadcidaddadariridciciarararcicaddcdiddddaridadcdaradad caaaagigiccaaarciggaagiccifgagacaaggaargiaarfggagagacagaggira 186 CAGGGCTGTTCAGAGCTTGAATACATGGCTGTTTATGTGTCGGATATTACAAATGCAGG 246 cresaacararcreaacrcacrreaasaaccrcrecrarrrescerrereridae 1535 CATGAAGAGAAGATAACTGATTTGCCACTTGACAATGGGGTGAGGGCTCTACTGAGGGG 485 GAGTCTGATGCATGCTACTGAATTCTCTACAGGTG---CCTAGTCTTCA-AAACTAGAT 1235 CAAAGGTGTCCCAAATCTGGAAGTCCTTGAGACAAGGAATGTAATTGGAGATAAGAGGTTA CTGGAACATATTGGAACTCACTTGAAGAACCTCTGTGATTTTCGCCTTGTGTTGCTTGAC Gaps 5, Score 464; DB 10; Length 574; Pred. No. 1.7e-76; 0; Mismatches 35; Indels 1775 ATGAGAGGTGTTTATTTT 1794 Query Match 20.3%; Best Local Similarity 92.9%; Matches 520; Conservative (1355 1475 9 1415 엄 д ద δ 음 Š Š ò à 셤 à 셤 à g Š 셤 8 g ò

Search completed: April 19, 2004, 20:29:44 Job time : 5817 secs

541 Argadaddararrirr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 19, 2004, 22:56:50; Search time 77 Seconds (without alignments) 2223.686 Million cell updates/sec Run on:

US-10-009-791-22 Title: Perfect score:

Sequence:

BLOSUM62

Scoring table:

1586107 segs, 282547505 residues

Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* .. Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2002s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	-		Arabi	Aab23457 Rice COII		4 Arabi	9 Ric	O. sat		Ara	-					-		Aab23455 Corn COI1		•	Arabid	_			Arabi	Aag78364 GRR1 homo
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6.2	0.9	5.9	5.6	9.5	ı,	5.4	5.4	5.4	4.	5.4	5.4	4.6	5.4	5.2	5.2	2.5	5.1	5.1	5.0
196	192	187.5	179	179	175	173	172.5	172	172	172	172	172	170.5	164.5	164.5	164.5	163.5	161.5	160.5
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ALIGNMENTS

RESULT 1

Corn; rice; soybean; wheat; ATHCOR1; LLS1; disease resistance; A. thaliana coronatine-induced; COI1; herbicides; EST; expressed sequence tag; sgs4c.pk003.k23:fis. AAB23458 standard; protein; 606 AA. (first entry) Soybean COI1 protein #2. 12-FEB-2001 AAB23458; AAB23458

Glycine max.

16-NOV-2000.

WO200068406-A2.

99US-0133041P. 03-MAY-2000; 2000WO-US011956. 07-MAY-1999; (DUPO) DU PONT DE NEMOURS & CO E I.

Maxwell CA; Lee J, Miao G, Famodu 00, Caimi PG,

New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides. 2000-687649/67. WPI; 2000-687649/ N-PSDB; AAA95063.

Claim 10; Fig 1; 74pp; English.

Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence is protein encoded by cDNA from the soybean clone sgs4c.pk003.k23:fis which is homologous to COII. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI DNAs of the invention may be used to alter the expression of COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides

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Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays Libs protein. The present sequence is the Arabidopsis thaliana COII protein. The COII and Libs proteins are involved in disease resistance. The COII and Libs proteins are particularly to produce transgenic plants with increased systemic particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and Libs proteins may be used to identify inhibitors of these proteins, which may be useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
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69.6%; Pred
72; 1
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                                                                                               Lee J,
                       03-MAY-2000; 2000WO-US011956
                                               99US-0133041F
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                                                                                                                       WPI; 2000-687649/67
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                                                  07-MAY-1999;
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16-NOV-2000
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AAB23466 RESULT

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Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLS1 protein. The present sequence is protein encoded by cDNA from the corn clone poll28.cpici34r:fis which is homologous to COII. The COII and LLS1 proteins are involved in disease resistance. The COII and LLS1 proteins are involved in disease the expression of COII and LLS1 protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLS1 proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays Libsi protein. The present sequence is protein encoded by cDNA from the rice clone flom.pk099.pl4:fis which is howologous to COII. The COII and LISI proteins are involved in disease resistance. The COII and LISI DNAS of the invention may be used to alter the expression of COII and LISI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LISI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
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                                                                                                                                                                                                                                  Corn; rice; soybean; wheat; ATHCOR1; LLS1; disease resistance; A. thaliana coronatine-induced; COI1; herbicides; EST; expressed sequence tag; f10n.pk099.pl4:fis.
NIELIPSRRVPEVNQOGEIREMEHPAHILAYYSLAGORTDCPTTV 585
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                                                                                           AAB23457 standard; protein; 597
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                          262 QGELTKYGNVKFPSRLCSLGLTYMGTNEMPIIFPFSALLKKLDLQYTFLTTEDHCQLIAK 321
                                                                                                                       New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
                                                                                               CPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDBEGTVSHRGLIALSQG
                                                                                                                                                                                                                                                                                                            506 GCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELL-PSRKVATNT
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9905-0142300F.
9905-0142803P.
9905-0142877P.
9905-0143542P.
9905-0143624P.
9905-0144005F.
9905-014408EP.
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                                                                                                                                                                                                                                                                        364 WVQGFRSSPIGTDIMAMVRPFWNIEYIV------PDQDEPCPEHKRQILAYYSLAGR 414
                                                     234
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                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                     64
                                                    176 KSLRVLFLEESSILEKDG-EWLHELALNNTVLETINFYLTDIAVVKIEDLELLAKNCPNL
                                                               GKUEL PIVEMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLFTRNVIGDRGLEVLGRC
                                                                                                                                                                  THLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIG
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                                                                                                                                                                                                                                      CKRLKRLRIERGDDDQ-GMEDEEGTVSHRGLIALSQGCSELEYMAVYVSDITNASLEHIG
                                                                                       235 VSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPE----RYSAISLPAKLCRIGITYI
                                     Gaps
                                     19;
                   39.2%; Score 1245.5; DB 3; Length 429; 57.5%; Pred. No. 6.9e-123; ive 69; Mismatches 95; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 36110.
                                                                                                                                                                                                                                                                                                                                                              AAG30234 standard; protein; 585 AA.
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99US-0123180P.
99US-0125788P.
99US-0125788P.
99US-0126264P.
99US-012624P.
99US-0128234P.
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99US-0130449P.
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                   Query Match
Best Local Similarity 57.5*
Matches 248; Conservative
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      Sequence 429 AA;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
06-APR-1999;
06-APR-1999;
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116-APR-1999;
21-APR-1999;
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RR 22-ULL-1999; 9903-0146463P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           GHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLET
                                                                                                                                                                                                                                                                                                                                                                                                                                         --FKVLVLTSCEGFSTDGIAAIAATCRNLRVLELRECIVEDLGGDWLSYFPESSTSLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 E--PERYSAISLPAKLCR----LGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : || :| :| || : || : || OLKPEAFSKLSBAFSNCKQLGSLSGLWDVLPEYLPALYSVCPGLTSLNLSYATVRMPDLY
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        32;
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25.7%; Score 818; DB 3; Length 585;
Best Local Similarity 34.6%; Pred. No. 3.4e-77;
Matches 200; Conservative 109; Mismatches 237; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 KVATNTNPDETVVVEHPA-HILAYYSLAGORSDFPDTV 595
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----DEHPPESRPESSPVERIYIYRTVAGPRMDTPEFV 568
99US-0159637P.
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99US-0160741P.
99US-016076P.
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AAB23449 standard; protein; 236 AA.

AAB23449

RXR

COII; rice, herbicide; disease-resistance factor.

AAP01920 standard; protein; 236 AA.

AAP01920

30-OCT-2001 (first entry)

AAP01920;

O. sativa COI1

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New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides.
                                   Corn; rice; soybean; wheat; ATHCOR1; LLS1; disease resistance; A. thaliana coronatine-induced; COI1; herbicides; EST; expressed sequence tag; contig.
                                                                                                                                                                                                    (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                           Claim 10; Page 44-45; 74pp; English.
                                                                                                                                                                    03-MAY-2000; 2000WO-US011956
       (first entry)
                                                                                                                                                                                                                    Famodu 00,
                                                                                                                                                                                                                                    WPI; 2000-687649/67.
                       Rice COI1 protein.
                                                                                                                                                                                                                                             N-PSDB; AAA95054.
                                                                                              Misc-difference
                                                                                                              Misc-difference
                                                                                                                                     WO200068406-A2
                                                                                                                                                                                     07-MAY-1999;
                                                                       Oryza sativa
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Maxwell CA;

Miao G,

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99US-0133041P

/note= "Encoded by GG"

Location/Qualifiers

'label= Unknown

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Expressed sequence tags (ESTs) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence is protein encoded by cDNA from the rice contig which is homologous to COII and LLSI proteins are involved in disease resistance. The coil and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to alter the expression of COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQKLEMRGC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 NLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 LFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVAT 562
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                                                                                                                                                                                                                                                                                                                                25.6%; Score 812.5; DB 3; Length 236; 66.8%; Pred. No. 3e-77; Indels 1. ive 30; Mismatches 47; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                            Matches 157; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                           Sequence 236 AA;
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RESULT

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An isolated polynucleotide (I) comprising a sequence (Ia) encoding a polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified composition of (IIa), is sequences, given in the specification, or the complements of (IIa), is and can be used, in sense or antisense orientation, to alter the composition of (II) in cells, particularly to produce transgenic plants with increased systemic resistence to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by can und/or identify specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as herbicides. This sequence is the rice COII protein created from a contign of rir2.pk0027.h4, r10n.pk099.p14 and rlon.pk0047.c5 as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 ELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 NLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDBEGTVSHRGLIALSQGCS
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                                                                                                                                                                                                                 'note= "encoded by ANG"
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                                                                                                                                                                                                                                                  /note= "encoded by GG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 44-45; 74pp; English.
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                       /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                Lee J,
                                                                                                                                                                                                                                                                                                                                          03-MAY-2000; 2000WO-US011956
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Matches 157; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                    Misc-difference 219
                                                                                                                                                                                         Misc-difference 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN02372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 236 AA;
                                                                                                                                                                                                                                                                                 WO200068406-A2
                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1999;
                                                                                                                                               Oryza sativa.
                                                                                                                                                                                                                                                                                                               16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Caimi PG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
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AAG3023
                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tags (ESTS) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence is protein encoded by cDNA from the wheat clone wreln.pk012.d3.fils which is homologous to COII. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequences engoding new disease resistance factors, inl for producing plants with increased resistance to pathogens and to ten for herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLOXLELRSCC-FSERALAVAALQLKSLRYLWVQGYKASPTGTDLMAMVRPFWNIEFIA- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLBFAKGCP 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLOKLEMRGCLFFSERALAVAATOLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GLMAVAEGCPDLEYWAVHVSDITNAALEAIGAFSKNLNDFRLVJLDREVHITELPLDNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
  LFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVAT 562
             C-FSEQALARAIRSMPSLRYVWVQGYKASKTGHDLMLMARPFWNIEFTPPRRLVT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                   Corn; rice; soybean; wheat; ATHCOR1; LLS1; disease resistance; A. thaliana coronatine-induced; COI1; herbicides; EST; expressed sequence tag; wreln.pk0122.d3:fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.5%; Score 716.5; DB 3; Length 221; 66.1%; Pred. No. 4.3e-67; ive 22; Mismatches 44; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 RKVATNTNPDETVVVEHPAHILAYYSLAGQRSDFPDTVVPL 598
                                                                                                                                                                                                                                                                                                                                               Maxwell CA;
                                                                                                                                                                                                                                                                                                                                                Miao G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 66-67; 74pp; English.
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                                                                              AAB23461 standard; protein; 221
                                                                                                                                                                                                                                                                                                                                                Lee J,
                                                                                                                                                                                                                                                                                 03-MAY-2000; 2000WO-US011956.
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                                                                                                                          (first entry)
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Best Local Similarity 66.1
Matches 146; Conservative
                                                                                                                                                Wheat COIl protein #4.
                                                                                                                                                                                                                                                                                                                                               Caimi PG, Famodu OO,
                                                                                                                                                                                                                                                                                                                                                                     2000-687649/67.
                                                                                                                                                                                                                 Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA95066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 221 AA;
                                                                                                                                                                                                                                     WO200068406-A2
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                                                                                                                         12-FEB-2001
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                                                                                                     AAB23461;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
               215
                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 36111
-----PNQDEP-CPEGGAQILAYYSLAGARTDCPQSVIPL
                                                                               Z
                                                                               AAG30235 standard; protein; 522
                                                                                                                                                                                                                                                                                                                                                                                             9905-0126264P.
9905-0126785P.
9905-0128714P.
9905-0128714P.
9905-0128714P.
9905-0138714P.
9905-0130449P.
9905-0130449P.
9905-013248P.
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99US-0137528P.
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99US-0137724P.
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99US-0135353P.
99US-0135629P.
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99US-0134941P.
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                                                                                                                                 (first entry)
                                                                                                                                                                                                                  rermination sequence.
                                                                                                                                                                                                                                        Arabidopsis thaliana
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17-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
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05-MAY-1999;
06-MAY-1999;
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18-MAY-1999,
                                                                                                                                   17-0CT-2000
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21-APR-1999;
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08-JUN-1
10-JUN-1
                                                                                                         AAG30235;
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                 182
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	, 678; DB 3; Length 522; No. 2.2e-62; smatches 219; Indels 32; Gaps
99US-0149175P. 99US-014972P. 99US-014972P. 99US-0149923P. 99US-0149923P. 99US-0149923P. 99US-0151065P. 99US-0151065P. 99US-0151065P. 99US-0151065P. 99US-0151066P. 99US-0151066P. 99US-015130P. 99US-015130P. 99US-015130P. 99US-015130P. 99US-015130P. 99US-0154018P. 99US-0154018P. 99US-0154018P. 99US-0154018P. 99US-0154018P. 99US-0155139P. 99US-0155139P. 99US-0155139P. 99US-0155139P. 99US-015529P. 99US-015529P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015928P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-015938P. 99US-016077P. 99US-016081P. 99US-016081P. 99US-016081P. 99US-016081P. 99US-016135P. 99US-016135P. 99US-016135P. 99US-016136P. 99US-016136P.	21.3%; Score Similarity 33.7%; Pred. 6; Conservative 96; Mie
PR 17-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 21-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 25-AUG-1999; PR 25-AUG-1999; PR 25-AUG-1999; PR 27-AUG-1999; PR 28-AUG-1999	Query Match Best Local Simil Matches 176; C

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RESULT 10 AAP0192 AAP01922

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expression of (II) in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by (I) are used to raise specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as herbicides. This sequence is the wheat COII clone created from contigs wreln,pk0122.d3 and wlln.pk0018.f8 as described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
                                                                                                                                                                                                                                                                                            438 RALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLBFAKGCP
                                                                                                                                                                                                                                                                                                                                                         378 GLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGV
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                     Length 177;
                                                                                                                                                                                                                                      36; Indels
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                                                                                                                                                                                                        DB 3;
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                                                                                                                                                                                                        19.3%; Score 613.5; DB 3 68.5%; Pred. No. 2.7e-56; ive 19; Mismatches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2000; 2000WO-US011956.
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                                                                                                                                                                                                                                             122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-687649/67.
N-PSDB; AAA95056.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COII protein
                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                           Sequence 177 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                              498
                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB23451;
                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t
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                                                                                                     316 TEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDBEGTVS 375
                                                                                                                                                                              293
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                                                                                                                                                                                                                                   315
          TVLETLNFYLIDIAVVKIEDLELLAKNCPNLVSVKLIDCEILD-LVNFFKHASALEEFCG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and screen for herbicides.
                                                                                                                                                                                                                                                                                                       DKGFKAIAEGCRDLRRLSV---SGLLSDKAFKYIGKHAKKVRMLSIAFAGDSDLMLHHLL
                                                                                                                                                                                                                                                                                                                                                                      DNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFA
                                                                                                                                                                            236 MPDLVELLRRCSKLOKLWVMDLIEDKGLEAVASYCKELRELRVFPSEPD--LDATNIPLT
                                                                                                                                                                                                               376 HRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLD--HEEKITDLPL
                                                                                                                                                                                                                                                                                                                                               494 KGCPSLOKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIE
                                                                            ---LGLTYIGKNELPIVFMFAAVLKKLDLLYAMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                     ::||:|| |:||
DEHPPESRPESSPVERIYIXRTVAGPRMDTPEFV 505
                                                                                                                                                                                                                                                                                                                                                                                                                   LIPSRKVATNTNPDETVVVEHPA-HILAYYSLAGORSDFPDTV 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COII; wheat; herbicide; disease-resistance factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 48-49; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 177
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9905-0134214P

9905-013424P

9905-0135623P

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18-MAY-1999;
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Expressed sequence tags (ESTS) from rice, wheat, soybean and corn cDNA libraries were found to be similar to cDNA encoding the Arabidopsis thaliana COII protein and the Zea mays LLSI protein. The present sequence is protein encoded by cDNA from the wheat contig which is homologous to COII. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI proteins are involved in disease resistance. The COII and LLSI protein in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. COII and LLSI proteins may be used to identify inhibitors of these proteins, which may be useful as herbicides
                                                                                                                                                               GLIALSQGCSELEYMAVYVSDIINASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGV 437
                                                                                                                                                                                                    RALLEGCDKLRRFALYLRRGGLIDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGCP 497
                                                                                                                                                                                                               61 RALLRGCTKIRRFAFYVRPGALSDLAFIXLGEFSKTVRYMLLGNAGSDDGLLAFARXCP 120
                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                       SLOKLEMRGCLFFSERALAVAATQLTSLRYLWVQSYGVSPSGRDLLVMARPFWNIELI 555
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                               1;
                                                                                                                              3; Length 177;
                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 36112.
                                                                                                                            19.3%; Score 613.5; DB 3 68.5%; Pred. No. 2.7e-56; ative 19; Mismatches 36
                                                                                                                                                                                                                                                                                                        AAG30236 standard; protein; 490 AA
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9905-012348P-
9905-0126264P-
9905-012678BP-
9905-012678BP-
9905-012678P-
9905-0128714P-
9905-013049P-
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                                                                                                                                      Best Local Similarity 68.53
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                            Sequence 177 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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21-APR-1999;
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13-0CT-1999;
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21-0CT-1999;
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24-SEP-1999;
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23-AUG-1999,
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415 CDFRLVLLD--HEBKITDLPLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSP 472
                                                                                                                                                                                                                                                                                                                                                                                              301 KCFRLCVIEPPAPDYKTNBFLDKGFKAIAEGCRDLRRLSV---SGLLSDKAFKYIGKHAK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                  417 CFVSFGACKLLSQKMPRLNVEVI-----DEHPPESRPBSSFVERIYIYRTVAGPRMDT 469
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                                                                                                                                                                                  126 IXSLHFRRMIVXDSDLQNLA---RDRGHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLF
                                                                                                                                                                                                                        LEESSILEKDGEWIHELALMNTVLETINFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDC
                                                                                                                                                                                                                                                                                                                RIRIERGDDDQGMEDEEGTVSHRGIJALSQGCSELEYMAVYVSDITNASLEHIGTHLKNL
                                                                                                                                                                                               243 BILD-LUNFFKHASALEEFCGGTYNEE--PERYSAISLPAKLCR-----LGLTYIGKNEL
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                 32;
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                                                                                                                                               Length 490;
                                                                                                                                                                 205; Indels
                                                                                                                                               18.2%; Score 579; DB 3; 33.1%; Pred. No. 6.6e-52;
                                                                                                                                                                   87; Mismatches
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99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0161404P.
99US-0161406P.
99US-0161359P.
99US-0161350P.
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Best Local Similarity 33.1;
Matches 160; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 VDVVLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                     Maxwell CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 555; DB 3;
Pred. No. 2.1e-50;
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                          /label= Unknown
/note= "Encoded by TTGC"
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                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 45-46; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP01921 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= unknown
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Best Local Similarity
  Misc-difference 97
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An isolated polynucleotide (I) comprising a sequence (Ia) encoding a polypeptide (II) of at least 60 amino acids (aa) from any of 18 specified sequences, given in the specification, or the complements of (Ia), is new. Herbicide. (I) encodes disease-resistance factor polypeptides (II) and can be used, in sense or antisense orientation, to alter the expression of (II) in cells, particularly to produce transgenic plants with increased systemic resistance to a wide range of pathogens. (I) or their fragments are also used for gene mapping (e.g. for plant breeding) and to identify loss of function mutants. Polypeptides (II) encoded by (I) are used to raise specific antibodies (for detection of (II)) and to design and/or identify specific inhibitors of (II), potentially useful as herbicides. This sequence is the soybean COII clone sgs4c.pk003.k23 as described in the method of the invention
                                                                                                                                                                                                                                                                           New nucleic acid sequences encoding new disease resistance factors, useful for producing plants with increased resistance to pathogens and to screen for herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 VDVVLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLE
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Best Local Similarity 96.3%; Pred. No. 2.1e-50;
Matches 104; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 SLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIV
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                                                                               Maxwell CA;
                                                                               Miao G,
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 45-46; 74pp; English.
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Sequence 6,
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-310-912A-2 US-08-41-08D-2 US-09-301-08D-2 PCT-US95-04570-2 PCT-US95-04570-2 PCT-US95-04570-2 US-09-252-991A-2974 US-09-245-92BA-19 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-245-92BA-18 US-09-181-770-7 US-09-181-770-7 US-09-458-791-2 US-09-458-791-2 US-09-458-791-2	ALIGNMENTS	Application US/09172841 223081 874ATUON: Harper, Jeffrey W. ELIGAGE, Stephen J. ELIGATION NUMBER: US/09/172,841 ING DATE: 1998-10-15 EQ ID NOS: 60 atentin Ver. 2.0 Homo sapiens 5.2%; Score 164.5; DB 3; Length 456; imilarity 23.8%; Pred. NO. 2e-09; Conservative 51; Mismatches 124; Indels 69; Gaps NIVASVKLTDCEILDLVNFFKHASALEEFCGGTVNEEPERYSAISLPAKL INTALDGSNWQRIDLFNFQIDVEGREVENISKEGGFLRKLSLRGCIGVGDSSLKTFAQN CRIP	CRNIEBHINLNGCTKÍTDSTCYSLSRFCSKÍKKHÍDÍJSCVSITNSSLKGISEGCRNLEYLN TRNVIGDRGLEVLGRCCKRLKRÍRIERGDDDQGMEDEEGTVSHRGLIALSQGCSELEY :	MAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDL - : : : :
8855 2 8855 3 8855 3 8855 3 8855 3 8855 5 88		Tion US/091 Jeffrey W. Stephen J. F-BOX PROT 1-03510 1 NUMBER: US 1: 1999-10-1 1 NUMBER: US 1: 1997-10-1 2S: 60 Ver. 2.0 Ver. 2.0 Jens 5.2%; 23.8%; 23.8%; 22.2%; 23.8%; 24.23.8%; 25.2%; 25.2%; 26.2%; 27.2%; 28.2%; 28.2%; 29.2%; 20.	NĠCŤKŤIDA RGLEVLGR(: DGIEALVR(NASLEHIG
		-841-51 No. 6232081 No. 6232081 ANT: Harper, Jeffrey W. ANT: Eledge, Stephen J. CEFERRES: ECM-03510 TAPPLICATION NUMBER: US/09/17 TELLING DATE: 1998-10-15 TR FILING DATE: 1998-10-15 TR FILING DATE: 1998-10-16 RE APPLICATION NUMBER: 08/951, RE FILING DATE: 1997-10-16 NO 51 HE: PAT OF SEQ ID NOS: 60 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 NO 51 HE: SEQ ID NOS: 61 HE: SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ ID NOS: 61 NO 51 HE: PAT OF SEQ ID NOS: 61 HE: PAT OF SEQ I	CRNIEHLNINĠCTKÍTDSTCYSLSR TRNVIGDRGLEVLGRCCKRLKRL : LSWCDQITKDGIERLVRGCRGLKAL	MAVYVSDIT
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450 FALYLRRGGIJDVGLGYIGQYSPNVRWMLLGYVGE-SDAGLLEFAKGCPSLQKLEMRGCL 241 LCL-SGCSNLTDASLTALGENCPREQILEAARCSHLTDAGFTLLARNCHELEKMDLEECT

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11 LSLRSNMTEERNVRKTRVVDVVLDCVIPY-
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                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 20.7
Matches 119; Conservative
Patent No. 6426205
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRNIEHLNLNGCTKITDSTCYSLSRFCSKLKHLDLTSCVSITNSSLKGISEGCRNLEYLN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 TR--NVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQGCSELEY 391
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2e-09;
                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                  Sequence 51, Application US/08951621
Patent No. 6573094
GENERAL INFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: ELLEDGE, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 164.5;
23.8%; Pred. No. 2e-0
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                                                                                                                                                                                                            CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: ECM-02999
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
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TYPE: amino acid
STRANDEDNESS: not releva
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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MOLECULE TYPE: protein

US-08-951-621-51
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Best Local Similarity
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US-09-177-165A-31
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; Sequence 31, Application US/09177165A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 DITESSDIKEGLQDLSRYSRQFINNVLSNPSNQNICTSVT----RRSPVFALNMLPSEI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 -HLESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 IHLILDKINQKYDIVKFLTVSKIMA-----EI----IVKILYYRFHINKKSQLDLF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ARDRGHVIHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNT 204
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APPLICANT: TYCER, Mike
APPLICANT: TYCER, Mike
APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTECLYSIS
FILE REFERENCE: 11757.10USUI
CURRENT APPLICATION NUMBER: US/09/177,165A
CURRENT APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-107-10
PRIOR FILING DATE: 1998-107-10
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 31
LENGTH: 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 VLETLNFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILDLVNFFKHASALBEFCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 GLI-ALSQGCSELEYMAVYVS-DITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%; Score 127.5; DB 4;
20.7%; Pred. No. 0.00018;
tive 78; Mismatches 190;
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ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                               1 Similarity 20.79
97; Conservative
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STATE: California
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                                                                                                      ORGANISM: Homo sapiens
US-09-172-841-53
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                                                       SEQ ID NO 53
LENGTH: 380
                                                                                                                                                                                                                                                                                                                                             92
                                                                                           TYPE: PRT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 KDGE---WLHELALNNTVLETLNFYLTDIAVVKIEDLELLAK---NCPNLVSVKLTDCEI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 DDDASSLILQLISLSELKT--FRLTS-SCVSTEGLAHLASGLGHCHHL-----E 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 KKLDLLYAMLDTEDHCMLIQRCPNLEVLET----RIVIGDRGLEVLGRCCKRLKRIRIER 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 KRLDLSHLLLNSSTLALLTHRLSOMTCLQSLRLNRNSIGDVG-----CCHLSEALR--- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GDDDQGMEDEEGTVSHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLDHE-----EKITDLPLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSP 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 DLSGNSISSAGGVQLAESIVLCRRLEELMLGCNAL------GDPTALGLAQ--ELPQ 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 LSLVGRP-AGLFSLRVQEPWADRARVLSLLEVCAQASGSVTEISISETQQQLCVQ-LEFP 168
                                                                                                                                                                                                                                                                                                                                equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GGHVTPWVKEISQYFDCLKSLHFR 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.7%; Score 119; DB 4; Length 483;
Best Local Similarity 21.7%; Pred. No. 0.00036;
Matches 96; Conservative 56; Mismatches 150; Indels 140; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 LDLSN------NQFDEEGTKALMRALEGKW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Harper, Jeffrey W.
APPLICANT: Halege, Stephen J.
TILLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION NUMBER: US/09/172,841
EARLIER APPLICATION NUMBER: 08/951,621
                          CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR PELICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLRVLHLPFSHLGPGGALSLAR 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-172-841-53
Sequence 53, Application US/09172841
Patent No. 6232091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 LKLKGKPRAAMFNL-IPEDW-
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa
NAME/KEY: SITE
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
             REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-904-615-154
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169 FHIGRECKSLRVLFLEESSILEKDGEWLHELALNNTVLETLNFYLTDIAVVKIEDLELLA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 -----DEHIGTHLKNL-----CD-----FRLVLLDHEEKITDLPLDNGVRA 439
                                                                                                                                                                                                                                                                                                                            124 ISVAGFSRFLKVCGSBLVRL------BLSCSHFLNETC-------LEVIS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 L--TYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
                                                                                                                                                                                                                                                                                                                                                                                            229 KNCPNLVSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPERYSAISLPAKLC---RLG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PPQAFNHI---AKLCSLKRLV 195
                                                                                           57 YELDSLITKKHVIIA-LCYITTPARLRR------RFPHLESLKLKGKPRAAMFNLIPEDW 108
                                                                                                                                                                                             109 GGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHVLHALKLDKCSGFTTDGL 168
                                                                                                                                                                                                                                285 TGCFTRLAHQLPNLQKLFLTANRSVCDTDIDELACNCTRLQQLDILGKVTI--
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  DB 3; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                 48 YELIQLILNHLTLPDLCRLAQTCKLLSQHCCDPLQYIHL-
                                                   65; Mismatches 131;
3.6%; Score 113.5; DB 3
20.7%; Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HARPER, JEFREY W.
APPLICANT: ELEBOOG, STEPHEN J.
THE OF TYPENTION: F-BOX GENES AND PROTEINS NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||| :: |: |: |
161 EMCPNLQALNLSSCDXL-----
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Patent No. 6573094
GENERAL INFORMATION:
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US-08-531-439B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 EMCPNIQALNISSCDKI--------PPQAFNHI---AKLCSIKKIV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L--TYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGL 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 EVLGRCCKRLKRLRIERGDDDGGMEDEEGTVSHRGLIALSOGGCSELEYMAVYVSDITNAS 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                           235 SMIGAKCKKLRTLDLWRCKN------ITENGIAELASGCPLLEELDLGWCPTLOSS
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                3.6%; Score 113.5; DB 4; Length 380; 20.7%; Pred. No. 0.00098; tive 65; Mismatches 131; Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 LLRGC--DKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGES 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08531439B
Patent No. 5881702
GENERAL INFORMATION:
APPLICANT: Zhang, Hui
APPLICANT: Beach, David
TITLE OF INVENTION: Cyclin/CDK Associated Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 18
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley, Hoad & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                 LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WAK-----
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 20.7*
Matches 97; Conservative
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ADDRESSEE: Foley, Ho
                                                                                                                                                                                            TOPOLOGY: not relevan

MOLECULE TYPE: protein

US-08-951-621-53
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US-08-531-439B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 ------LAKN-SNLVRLNLPGCPGFPKFPLQTFLSSCPRLDELNLSWC-FNFTEK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 HVQVAVAHVSETMTQLNLSGYRKN-----LQKSDL-----STLVRRCPN 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 VSGVCKRWYRLASDESL-----NLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 KLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETLNFYLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 VSQVCRRWYEL---DSLTRKHVTIALCYTTTPARLRRRPHLESLKLKGKPRAAMFNLIP
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Sequence 2, Application US/09331403
Patent No. 6489147
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALTMANN-JOHL, Regula; PHILIPPSEN, Peter; ALTHOFER, Heming; SEULBERGER, Harald.
TITLE OF INVENTION: Adenylate cyclase gene, and its use NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM AT-compatible, Pentium III processor OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect version 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.5%; Score 112.5; DB 2; Length '
Best Local Similarity 23.2%; Pred. No. 0.0016;
Matches 72; Conservative 34; Mismatches 75; Indels
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RAPLICATION NUMBER: US/09/331,403
APPLICATION NUMBER: US/09/331,403
ALILING DATE: 21-Jun-1999
CLASSIFICATION: «UNKNOWIN»
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/531,439B
FILING DATE: 21-SEP-1995
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-006.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LIENGTH: 435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 LEVLETRIVI 338
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COUNTRY: USA
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; Sequence 12, Application US/08462467B
; Sequence 12, Application US/08462467B
; Patent No. 6210899
; GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I
TITLE OF INVENTION: BMP Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLOILDISGCT--SLQGLPDSVGQLTGLRTLHLENCTSLQGLPDSVGNLTSLK---WLNL 482
                                                                                                     133 L---WQHE---SQAPLQLTELYIDATLSBVPQSIGKLNQLERIVLKNGYFKTLPNEFYDM 186
                                                                                                                                                       234 --INSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPERYSAIS----LPAKLCRL-GL 286
                                                                                                                                                                                                                                        287 TYIGKNE-----LPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGD 340
                                                                                                                                                                                                                                                                                                                                                               398 DITNA-----SLEH1-----GTHLKNL--CDFRLVLLDHEEKITDLPLDNGVR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 QITGLEGLYLSGCFSLQGLPDSVGQLTGLQSLNLEYCTSLEGLPDSVGQLTDLPILD--- 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                               187 HSLKHITLQNCEQMML----LPDSVGILTGRQTHDFSGCSNLQALPDSVGQLTGL 237
                                                                                                                                                                                                                                                                                238 KTLDLEDCTSLQGLPDSVGQLTGLQSLDL-----EHCTSLQGLP-----DSVGQ 281
                                                                                                                                                                                                                                                                                                                          -RGLEVLG-RCCKRLKRLFIERGDDDQGMEDEEGTVSHRGLIAL-SQGCSELEYMAVYVS 397
                          73 İSRİELLRGEGSFVESIFSAĞEIRQLVYLQWKECPISSISFTIPTRNİSVLYIQGYALKT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 ALLRGCDKLRRFALYLRRGGLTDVGLGYI-GQYSPNVRWMLLGYVGESDAGLLBFAKGCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 --INTCISLQ------GLPD-SVGQLRGLQNLDLRWC------DSLQGLPDSVGQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 SLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQG----YGVSPSGRDLLVMARPFW---
                                                                          91 KDGEWLHELAINNTVLETLNFY----LTDI--AVVKIEDLELLA-----KONCPN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEER: The Procter & Gamble Com. 1. 11810 East Miami River Road Ross
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APPLICATION NUMBER: US/08/462,467B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 5474
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
TELEPAX: (513) 627-0260
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
152 LHALKLDKCSGFTTDGLFHIGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Herbko, Bart S.
REGISTRATION NUMBER: 32,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 ----NIELIPS 557
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45061
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US-08-462-467B-12
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APPLICANT: LASHAM, Annette
APPLICANT: LASHAM, Annette
APPLICANT: LASHAM, Annette
APPLICANT: LASHAM, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
TITLE OF INVENTION: 4090-06-04
UNDRER OF SEQ ID NOS: 206
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 -VIKKLDLLYAMLDTEDHCMLIQRCPNLEV--LETRNVIGDRGLEVLGRCCKRLKRLRI- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 -ERGDDDQGMEDEEGTVSHRGLIALSQGCSELEY-MAVYVSDIT---NASLEHI---- 407
                                                                                                                                                                                                                                                                                                                                         138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
                                                                                                                                                                                                                                                                                                                                                                 S--DLONLAR---DRGHVLHALKLDKCSGFTTDGLFHIGRF-----CK--SLRVLFLE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 ES--SILEKDGEWLHELALNNTVLETL---NFYLTDIAVVKIEDLEL-----LAKNCPN 233
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                                                                                                                                                                                                                                                                                                                                         79 RIRRREPHIESIKUKGKPRAAMFNIIPEDWGGHVTPWVKEISQYFDCIKSIHFRRMIVKD
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GT--HLKNLCDFR----LVLLDHEEKITDLPLDNGVRALLR 442
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3.5%; Score 110.5; DB 4; Length 579;
Best Local Similarity 22.0%; Pred. No. 0.0046;
Matches 108; Conservative 70; Mismatches 158; Indels 155;
                                                                                                                                                                                                                                                                                                 Indels 133;
                                                                                                                                                                                                                                                          DB 4; Length 1874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 LVSVKLTDCEILDLVNFFKHASALEEFCGGTYNEE--PERYSAI-----
                                                                                                                                                                                                                                                          Query Match 3.5%; Score 111.5; DB 4; Best Local Similarity 22.7%; Pred. No. 0.029; Matches 107; Conservative 71; Mismatches 160;
    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/07309
FILING DATE: 29-DEC-1997
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-325-932A-185
Sequence 185, Application US/09325932A
Patent No. 6451604
                                                                                                           LENGTH: 1874 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 PAKLCRLGLTYI-----
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US-09-325-932A-185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 YIGKNELPIVFMFA----AVLKKLDLLYA--MLDTEDHCM--LIQRCPNLEVLETRNVIG 339
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                                                                                                                     --- LPHIGRECKSLRVLFL--EESSILEKDGEWLHELALNNTVLETLNFYLTDIAVV 219
                                                                                                                                                                   369 LALRDELPAALLASTPRLVILNAWTLLYAGRLAEAED-CIGQLARFLEMPSASRQRVLLA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597
--LHFRRMIVKDSDLQ----NLARDRGHVLHALKLDKCSGFTTDG 167
                                          ---LIDCEILDLVNFFKHASALEEFCGGTYNEEPERYSAISLPAKLC------RLGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 D-RGL-EVLGRCCKRLKRLRIERGDDD-----QGMED--EEGTVSHRGLIALSQGCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 ----LRGCDXLRRFALYLRRGGLTDVGLGY---IGQYSPNV-RWMLLGYVGESDAGLLBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 MDQARLIGRDALRLAREHDSLIFEALIELERAQWLEORGELLRAEGVLDRAQRYLEDLGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 LEYMAVYVSDITNASLEHIGTHLKNLCDF-RLVLLDHEEKI--TDLPLDNGVRAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536 SPSGRDLLVMARPFWNIELIPSR-KVATNTNPDETVVVEHPAHILAYYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 GOGDLDAAFNRLLEVERLMQQRHVPDPLYRGALLLVSSALTLQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Materials for
Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Michelmore, Richard W.
APPLICANT: Michelmore, Richard W.
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in ITLE OF INVENTION: Conferring Pest Resistance in INUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Bighth Floor CITY: San Francisco
STREET: California
COUNTRY: USA
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                                                                                                                                                                                                                                                    -----KIEDL----ELLAKNCPNLVSVK--
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PRIOR APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ARGUINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/0074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PELING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 CPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 KLRRFALYLRRGGLTDVGLGYIGQYSPNVRWML--LGYVGESDAGLLEF-----AKG 495
                                                                                                                                                                                                                                                                                                                            GLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETLNFYLTDI-----AVVKI 221
                                                                                                                                                                                                                                                                                                                                                                                          831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SERALAALA-- 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 ----SPSGR---DLLVMARPFWNIELIPSRKVATNTNPDETVVVEHPAHILAYYSLAG 586
                                                                                                                                                                                                                                                                                                                                                                      || || :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----BLYSCYSALATH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 CSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLELLA------KNCP----NLVSVKLTDCEILDLVNFFKHASALEEFCGGTY
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 CPSLOKLEMRGCL----FFSERAL-----AVAATOLISLRYLWVQGYGV----
                                                                                                                                                                                                   ; Score 109; DB 3; Length 1495; ; Pred. No. 0.038; 44; Mismatches 164; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%; Score 108; DB 4; Length 870; 21.6%; Pred. No. 0.019; Live 79; Mismatches 240; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            956 C----YSGLYLECYSHISLEHISTH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 --RLEASPTHRARGALALELELYSLEALATYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28407, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                    STRANDEDNESS: not relevant
TOPOLOGY: not relevant
WOLECULE TYPE: protein
                                                                                                                                                                                                             3.4%;
ilarity 22.3%;
Conservative 44
LENGIH: 1495 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     890 SERLETYRA-SPPHEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                              Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-28407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-252-991A-28407
                                                                                                                                  , MOLECULE TYPI
US-08-462-467B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                              222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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291 --KNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGR 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IPEDW-GGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 PVTMSGDVLDQIYLSNNWFSGEIPPAIGN----PPNLQTLFLDRNRFRG----NIPREIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 --FAGNTYLCLPHRVSCPTRPQQTSDHNHTALFSPSRIVITVIAAITGLILISVAIRQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 KKKNOKSLAWKLTA-FOKLD-----FKSED------VLECLKEENIIGKGGSGIVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 FILQLPANLGRNGNLIKLDVSDNHLTGLI-----PKD------LC-RGEKLEMLILSNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 N-NVKNLGTLNISGNQLTGSIPTGIGNMTSLTTLDLSFNDLSGRVPLGGQFLVFNETS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 FFGPIPEELGKCKSLTKIRIVKNL-----LNGTVPAGLFNLPLVTIIELTDNFFSGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 HVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 DITNASLEHI-----GTHL------KNLC----DFRLVLLDHEEKITDLPLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 FTLSLRSNMTEERNVRKTRVVDVVLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 NFYLTDIAVVKIEDLEL---LAKNCPNLVSVKLTDCEILDLVN-----FFYGHASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 GVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLE 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%; Score 103.5; DB 2; Length : 19.6%; Pred. No. 0.075; tive 77; Mismatches 215; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                      SOFIWARS: FACERLIN RELEASE #1.0, VETSION TO SET OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 980 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.3%
Best Local Similarity 19.6%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-473-553A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 TVSHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLP 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 VKDSDLQNLARDRGHVLHALKLDKC-----SGFTTDGLF------HIGRFCKSLRV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LFLEESSILEKDGEWIHELALNNTVLETINFYL--TDIAVVKIEDLELLAKNCPNLVSVK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 LVRAFVLDTFNRFKHSLIVNHGNGGMLG-WPEN----DMSASSCKRISLICKGMSDFPRD 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 IDNGV---LKKLVKLEE--LYMRVGGRYQKAISF-------TDENCNEM 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 IEHHDIETIA----HVVFQMSYDNLQNEEAQSIFLLCGLFPEDFDIPTEELVRYGWGLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTDCEILDLVNFFKHASALEEFCGGTYNEEPERYSAISLPAKLC-RLGLTYIGKNELPIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 FMFAAVL------MLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 VKFPNLLILKLMHADKSLKFPQDFYGEMKKLQVISYDHMKYPLLPTSPQCSTNLRVLHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCP-----NLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585 QCSLMFDCSSIGNLLNLEVLSFAN----SGIEWLPSTIGNLKELR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 LDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.3%; Score 104; DB 4; Length 1074;
Best Local Similarity 20.6%; Pred. No. 0.078;
Matches 91; Conservative 41; Mismatches 124; Indels 186; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 F----NGVYTIGEARHRINAYIELLKDSNLLIESDDVHCIKMHD
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APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "RG2K deduced sequence'
NAME: Binhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFENCE/DOCKET NUMBER: 023070-078810US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 111:
REQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKGCPSLOKLEMRGCLFFSERA 514
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..1074
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OTHER INFORMATION:
US-09-004-838-111
                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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US-08-473-553A-6
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788 YLFTVYLGA----EGFVEKTEMKGIE-EVVKLYMDDLISSSLV--IC--FNEIGDILNFQ 838
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                                        114 GSMPNNVDVAIKRL-VGRGTGRSDHGFTAEIQTLGRIRHRHIVRLLGYVANKDTNLLLYE 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FLFTLSLRSNMTEERNVRKTRVVDVVLDCVLPYIDDPKDRDAVSQVCRRMYEL-DSLTRK
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349 CCK-----RIKRIRIERGD--DDQGMEDE---EGTVSHRGLIALSQGCSELEYMAVYVS
                                                                                                                                                                 APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Valerie M.
APPLICANT: Xaloshian, Isgouhi
APPLICANT: Yadiosbi, Jafar
APPLICANT: Yadiosbi, John
APPLICANT: Milligan, Stephen
APPLICANT: Bodeau, John
APPLICANT: Brocedures and Materials for Conferring
TITLE OF INVENTION: Pect Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE S:
CORRESPONDENCE TOWNSENG and TOWNSENG and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHARRE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-947-823-5
'Sequence 5, Application US/08947823
'Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1257 amino acids
                                                                                                                                         398 DITNASLEHI-----GTHL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 107; Conservative
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STREET: Two Embarcad
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
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19.9%; Pred. No. 0.086;
tive 71; Mismatches 191; Indels 174;
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                                                                                                                                                                                                                                                                                                                                  CORDENOIS ADDRESS:
ANDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                            APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                 Sequence 2, Application US/08473553A Patent No. 5859338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                              GENERAL INFORMATION:
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Search completed: April 20, 2004, 01:39:25 Job time : 28 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655, App
268553,
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                                                                            April 20, 2004, 01:38:26 ; Search time 362 Seconds (without alignments) 461.486 Million cell updates/sec
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1 TKTSAPFLFTLSLRSNMTEE.....QRSDFPDTVVPLDTATCVDT 606
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                 1124875 seqs, 275673149 residues
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ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Chou, Yihua

APPLICANT: Covalic, David K.

APPLICANT: Screen, Steven B

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

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APPLICANT: Tabaska, Jack E

APPLICANT: S1014

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 18/10/425,114

CURRENT FILING DATE: 2003-04-28

KUMBER OF SEQ ID NOS: 73128

SEQ ID NO 45837

LIBUGHE S22
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97.9%; Score 3112; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-307;
Matches 592; Conservative 0; Mismatches 0;
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US-10-425-114-45837
Sequence 45837, Application US/10425114
Publication No. US20040034888A1
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300 376 360 480

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181 HELALMNTVLETLNFYLTDIAVVKIQDLELLAKNCPNLVSVKLTDCEVLDLVNFFKHASA 240
                                             EDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSH
                                                                                           RGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLFLDNG
                                                                                                                                              437 VRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGC
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                                                                                                                                                                                                                                                                                        Sequence 520, Application US/10310154 Publication No. US20030233670A1 GENERAL INFORMATION:
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Parnell, Laurence D.
Start, William G.
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
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Jung, Vincent
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Deikman, Jill
Deng, Molian
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Hinchey, Brenda S.
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Lund, Adrian
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Kretzmer, Keith A
Laccetti, Lucille
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Stephen M.
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Ruff, Thomas G.
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
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Publication No. US2004003107241

Publication No. US2004003107241

APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei

TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 284666

LENTH: 590
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                                                              SALBEFCGGTYNEEPERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKLDLLYAML
                                                                                                                                                                   GCPSLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIEL
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                                                                                                                                                     DTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTV
                                                                                                                                                                                                        SHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLD
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                                                195 WIHELALINNTVLETINFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILDLVNFFKHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITHER INFORMATION: Clone ID: PAT_MRT3847_99079C.1.pep. US-10-424-599-284666
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-424-599-284666
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                                                                                                                                                                                                                                                                                                 56.2%; Score 1786.5; DB 15; Length 598; 60.1%; Pred. No. 1.7e-172;
                               APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REPERENCE: 39 1-5 (52796) B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR PILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
LENGTH: 598
                                                                                                                                                                                                                                                                                                                                  85; Mismatches 136; Indels
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Best Local Similarity 60.1%
Matches 349; Conservative
Zeng, Xiaoping
                  Zhang, Qiang
Zhao, Yajuan
Zhou, Li
                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Zea mays
US-10-310-154-520
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Sequence 519, Application US/10310154
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas H
APPLICANT: Agarwal, Ameta K.
APPLICANT: Agarwal, Ameta K.

US-10-310-154-519

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80 ESLKLKAKPRASMFNLISDDWGGSASPWIRQLSATFHFLKKLHLRRMIVSNEDINILVRA 139
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APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhang, Qiang
APPLICANT: Zhang, Qiang
APPLICANT: Zhou, Li
TITE OF INTURNITON: Gene Sequences and Uses Thereof in Plants
FILE NEFERENCE: 38-15 (52795)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT TILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR PLICATION DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 519
LERNGHH: 531
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                                                                                                                                                                                                                                                                                                                                                                                                            Padmavathi, Manchikanti
Parnell, Laurence D.
Start, William G.
Tennesen, Dan
Vidya, K.R.
Wang, Haniyun
Xin, Zhanguo
                                                                                                                                                                                                                                                                                                                                              Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Bell, Erin
Boddupalli, Raghava
Boddupalli, Raghava
Deix, Molian
Dong, Jinzhuo
Duff, Stephen M.
Galligan, Meghan M.
Hinchey, Brenda S.
                                                                                                                                                         Johnson, G. Richard
Jung, Vincent
                                                                                                                                                                                         Kretzmer, Keith A
Laccetti, Lucille
Lai, Chao-Qiang
                                                                                                                                                                                                                                                                                              Lu, Bin
Luethy, Michael M.
Lund, Adrian
                                                                                                                                         Shihshieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330; Conservative
                                                                                                                                                                                                                                                          Lin, Jie-Yi
Liu, Jingdong
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US-10-310-154-519
                                                                                                                                               Huang,
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Best Local S:
Matches 330
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Expure Expured K.
APPLICANT: Sovalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: UC-ZMFLB73276H05_FLI.pep
US-10-425-114-56666
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; Sequence 69709, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
                                                                                                                          Sequence 56666, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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   909
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LENGTH: 425
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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|: : PAGGPVASRNYENYYFPPSLHHLSLLYMGTNDMQILFPYATALKKLDLQFTFLSTEDHCQ 318
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                                                                                                                                 ALSOGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRAL
                                                            LIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQ-GMEDEEGTVSHRGLI
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Best Local Similarity 100.0%; Pred. No. 2.7e-152;
Matches 302; Conservative 0; Mismatches 0; Indels 0.
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US-10-425-114-49508
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10-425-114-49508
10-10-425-114-49508
1 Sequence 49508, Application US/10425114
1 CARREAL INFORMATION:
1 APPLICANT: Liu, Jingdong
1 APPLICANT: Zhou, Yihua
1 APPLICANT: Sovenic, David K.
2 APPLICANT: Sovenic, David K.
3 APPLICANT: Tabaska, Jack E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Can Vinua
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APPLICANT: Can Vinua
APPLICANT: Can Vinua
APPLICANT: Can Vinua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245726
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                                                                                                                                                                                                                                                                                                                    RGLBVLGRCCKRLKRLRIBRGDDDQGMBDBBGTVSHRGLIALSQGCSBLBYMAVYVSDIT 400
                                                                                                                                                                                                                                                                                                                                            461 DVGLGYIGQYSPNVRMMLLGYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAAT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 SMPSLRYVWVQSYKASQTGRDLMLMARPFWNIEFTPPSSQNAGRLIEDGEPCVDSHAQIL 372
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                                                                                                                                                                                                                                    281 LCRLGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGD
                                                                                                                                                                                                                                                            401 NASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALYLRRGGLT
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                                                                                                                                                                              14 DLELLAKSCKSLISLKIGDCDLSDLIGFFQSATSLEBFAGGTFNGQGBLTKYGDVKFPSR
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                                                                         Length 394;
                                                                                                                                                           223 DLELLAKNCPNLVSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPE
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al Similarity 33.2%; Score 759.5; DB 12; Length
194; Conservative 95; Mismatches 256; Indels
                                                                                                                    Indels
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                                                                           37.5%; Score 1193; DB 12;
61.7%; Pred. No. 2.6e-112;
tive 57; Mismatches 84;
; FEATURE:
; OTHER INFORMATION: Clone ID: 700800510_FLI.pep
US-10-425-114-46788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 245726, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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                                                                                  Query Match
Best Local Similarity 61.74
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-10-424-599-245726
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Matches 19
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APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DAIDS: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                              APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cap. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERROR: 38-21/53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 69709
LENGTH: 410
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                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: UC-ZMFLMO17190F07_FLI.pep
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                         Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Expusive to bavid K
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 212007
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                                                                                                                                                                            -PERYSAISLPAKLCR----LGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCML 322
                                                                                                                                                                                                                 252 RPEVFSNLEAAFSGCKQLKGLSGFWDVLPSYLPAVYPICSRLTSLNLSYAIIQSSDLIKL 311
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                134 KVLVLTSCEGXTPLGLAAIAANCRNLRELDLQESEV-EEDLCGHWLSHFPDSYTSLVSLN 192
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                                                                                                           ISCLN-NEVSLSALERLIGRCPNLRTLRLNRAVPLDRLPNLLLRAPQLVELGTGVYSTEM
                                                                   211 FYLTDIAVVKIEDLELLAKNOPNLVSVKLTDCEILD-LVNFFKHASALEEFCGGTYNEE-
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APPLICANT: La Rosa Thomas J
APPLICANT: Xovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
210 NFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILD-LVNFFKHASALBEFCGGTYNEE 268
                                                                                                                                                                                        269 PERYSALSLPAKLCRL-----GLTYIGKNELPIVFMFAAVLKKLDILYAM-LDTEDHC 320
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23.2%; Score 737; DB 12; Length S8
Best Local Similarity 32.7%; Pred. No. 1.4e-65;
Matches 188; Conservative 108; Mismatches 253; Indels
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US-10-424-599-234595
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OTHER INFORMATION: unsure at all Xaa locations
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US-10-424-599-234595
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Length 597;

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Agarwal, Ameeta K.

; Sequence 68189, Application US/10425114; Publication No. US20040034888A1

APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua

GENERAL INFORMATION:

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Page 7

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBRICE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 68189
LENGTH: 597
TYPP
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21.7%; Score 690.5; DB 12; Length
Best Local Similarity 31.2%; Pred. No. 7.8e-61;
Matches 181; Conservative 114; Mismatches 251; Indels
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US-10-425-114-68189
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APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Show Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERROTH: 218
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US-10-424-599-143159
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ORGANISM: Glycine max
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Sequence 268553, Application US/10424599
; Sequence 268553, Application US/10424599
; Publication No. US20040031072A1
; Publication No. US20040031072A1
; APPLICANT: La Rosa Thomas J
APPLICANT: La Royalic David K
APPLICANT: Zhou Yihuas J
APPLICANT: Zhou Yihuas J
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 26853
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                                258 HLGTGSFRPADGGEBGTGFGEVVSAFVAAGRARTLVSLSGFRDLAQEYLPTIAVVCAHLK 317
                                                                                                    366 GMEDEEGTVSHRGLIALSÇGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLL--- 422
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                                                                           306 KLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQ
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20.6%; Score 655.5; DB 12; Length 150;
Best Local Similarity 82.7%; Pred. No. 3.3e-58;
Matches 124; Conservative 10; Mismatches 15; Indels 1;
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US-10-424-599-268553
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OTHER INFORMATION: unsure at all Xaa locations
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NAME/KEY: unsure
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Best Local Similarity 31.4%; Pred. No. 2.1e-59;
Matches 187; Conservative 91; Mismatches 270; Indels 47;
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CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR PELICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
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Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
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Duff, Stephen M.
Galligan, Meghan M.
Hinchey, Brenda S.
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Jaccetti, Lucille B.
                                                                                                                                                                                                                             Huang, Shihshieh
Johnson, G. Richard
Jung, Vincent
                                                                                          Boddupalli, Raghava
Deikman, Jill
Deng, Molian
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Start, William G.
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Zeng, Xiaoping
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
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Zhao, Yajuan
Zhou, Li
                                    Ball, James A.
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Bin
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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April 19, 2004, 22:59:35 ; Search time 19 Seconds (without alignments) 1660.764 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-009-791-22 3180 1 TKTSAPFLFTLSLRSNWTEE......QRSDFPDTVVPLDTATCVDT 606 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P34284 caenorhabdi	hom	ET III	mus n	homo	9 homo	schi			_	9	9 sacch						caenc	4 homo	homo	พน ย	homo	homo	mus		haem (DEOU.		ш	aduitex	_	9564	P47637 mycoplasma
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	Score	183.5		175	175	172	170.5		147.5	141	139	133	132	131.5	127.5	126.5	120.5	119	118	117.5	115	114.5	110.5	110.5	109	108	106.5		0.5	104.5	103	103	103	102.5
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Q9npp4 homo sapien P42500 glycine max O88520 mus musculu P03875 saccharomyc P10775 sus scrofa P13489 homo sapien Q21444 caenorhabdi Q9bxb1 homo sapien Q3zci7 ricketteia Q3zci7 ricketteia Q01082 homo sapien Q9c646 arabidopsis	
CARC HUMAN PHYA_SOYEN SHOZ MOUSE ALIM_YEAST RINI_PIG RINI_PIG COG2_CAEEL LGR4_HUMAN COG2_CAEEL LGR4_HUMAN SCHPO AK RICPR SPCO_HUMAN RZ4L_ARATH	
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ALIGNMENTS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                       LER 1.
LER 2.
LER 3.
LER 3.
LER 4.
LER 5.
LER 6.
LER 8.
LER 9.
LER 9.
LER 1.
LER 11.
                                    PROSITE; PS50181; FBOX; 1.
Hypothetical protein; Ubl conjugation pathway; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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22.0%; Pred. No. 1.2e-06;
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Last annotation update)
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15-MAR-2004 (Rel. 43, Last ann
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SMART; SM00367; LRR_
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Local Sim
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Q961G2;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Batchenko L., Marusina K.P., Parmer D., Wang J., Halseh F., Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., R.A. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Parage C., Raha S.B., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.W., R.A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R.A. Hillalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A., Hillalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A., R. Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A. R. Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., R. Babeseley R.W., Touchman J.W., Green E.D., Dickson M.C., R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; R. Generation and initial analysis of more than 15,000 full-length proceins and promotes that ubiquitination and degradation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 179; DB 1; Length 43
22.5%; Pred. No. 2.5e-06;
Live 47; Mismatches 114; Indels
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Pfam; PF00560; LRR; 2.
SWART; SW00256; PB0X; 1.
SWART; SW00367; LRR CC; 12.
PROSITE; PS50181; FB0X; 1.
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InterPro; IPR001611; LRR.
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Last annotation update)
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115-MAR-2004 (Rel. 43, Last sequ
15-MAR-2004 (Rel. 43, Last sequ
                                                                               EMBL, AK039010; BAC30203.1; -. EMBL, AK044693; BAC32036.1; -. EMBL, AK045742; BAC32477.1; -. EMBL, AK08994; BAC41033.1; -. MGD; MGI:1919429; Fbx12.
                                                                                                                                                                     InterPro; IPR001810; F-box.
InterPro; IPR001611; LRR.
InterPro; IPR00169; LRR.
Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46890 MW;
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A Okazaki Y. Puruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Jadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baladarelli R., Hill D.P., Bult C., Godzik A., Gough J.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani D.E., Cousins S.,

A Dalla E., Dragani T.A., Fletcher C.F., Fortsest A., Frazer K.S.,

A Gassterland T., Gariboldi M., Hirokawa N., Jackson I.J., Jarvis E.D.,

A Annai A., Kawaji H., Kawasawa Y., Kediterski R.M., King B.L.,

A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mit H.,

A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mit H.,

A Maglott D.R., Manger K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

A Shitana R., Magner L., Wahlestett C., Wang Y., Watanabe Y., Walls C.,

A Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

A Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Rayawa I.,

A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sahiraki T., Waki K., Kawai J., Aizawa K., Airkawa T., Fukuda S.,

A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

A Minaki K., Kawai J., Shibata K., Shinagawa A.,

A Mara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

A Washiishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

A Washiishi A., Sakaini K., Sasaki D., Shibata K., Shinagawa A.,

A Washuishi A., Yoshino M., Waterston R., Lander E.S., Roorers J.
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 270 ERYSAISLPAKLCRIGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNL 329
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OBEXM4;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
F-box/LRR-repeat protein 2 (F-box and leucine-rich repeat protein 2).
FBXL2 OR FBL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 420:563-573 (2002).

-[-FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

-[-SUBUNIT: Interacts with SKPI. Part of a SCF (SKPI-cullin-F-box) protein ligase complex (By similarity).

-[-SIMILARITY: Contains 1 F-box domain.
-[-SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/63; TISSUE=Brain, Hypothalamus, and Retina;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                    447 LRRFALYLRRGGLTDVGLGYIGQYSPNVR 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAAMFNLIPEDWGGHVTPWVKEISQYFDC---LKSLHFRRMI-VKDSDLQNLARDRGHVL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EEFCGGTYNEEPERYSAISLP--AKLCRLGLTYIGKNELPIVFMFAAVLKKLDLL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 YAMLDTEDHCMLIQRCPNLEVLETRNV--IGDRGLEVLGRCCKRLKRLRIERGDDDQGME 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVDLFN-FQTDVBGRV---VENISK--RCGGFLRKLSLRGCIGVGDSSLKTFAQNCRNIE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 HALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEES-SILEKDGEWLHELALNNTVLFTLNF 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 SWCD--QITKEGIEALVRGCRGLKALLLRGCTQLEDEALKHIQNHCHELVSLNLQSCSRI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEEGTVSHRGLIALSQGCSELEYMAV-YVSDITNASLEHIGTHLKNLCDFRLVLLDHEEK 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 YLTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILD---LVNFFKHASAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> S (IN REF. 1; BAC32036).
597713D0407195CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 TDDGVVQICRGCH----RLQALCLSGCSNLTDASLTALGLN-~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubl conjugation pathway, Leucine-rich repeat, Repeat. DOMAIN 9 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9e-06;
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                                                                                                                                                                                                                               RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ra Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Ra Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Golobori T., Bono H., Ksukwa T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ra Fleischmann W., Garbuli F., Towita M., Wagner L., Washio T., Ra Kuchl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ra Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A. Lyone P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P., Rasaki H., Sato K., Stonbach C., Seya T., Sikamoto N., Storch K.F., Sasaxi H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., M. Hayshiazaki Y., Loshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayshiazaki Y., Landarian M., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayshiazaki Y., Landarian M., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayshiazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";

Nature 409.685-690(2001).

-!- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.

-!- SUBUNIT: Interacts with SKPI. Part of a SCF (SKPI-cullin-F-box) protein ligase complex (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00256; FBOX; 1.
SMART; SM00367; LRR CC; 2.
PROSITE; PS50181; FBOX; 1.
UD1 conjugation pathway; Leucine-rich repeat; Repeat;
Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9CZV8-2; Sequence=VSP_008968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9CZV8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK012109; BAB28039.1; ALT_INIT.
EMBL; AK036217; BAC29349.1; -.
MGD; MGI:191944; 2610511F20Rik.
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LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
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InterPro; IPR001611; LRR.
InterPro; IPR007089; LRR_Cys.
InterPro; IPR006553; LRR_Cys_sub.
       F-box/LRR-repeat protein 2-like
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Pfam; PF00560; LRR; 2.
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                                                       Mus musculus (Mouse)
                                                                                                                                NCBI_TaxID=10090;
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151 VLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETLN 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20399565; PubMed=10945468; Ilyin G.P., Rialland M., Pigeon C., Guguen-Guillouzo C.; "cDNA cloning and expression analysis of new members of the mammalian F-box protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 ERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 -----SLCASGCSNITD----ALLMALG------QNCPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 EVLETR---NVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQGCS
                                                                                                                                                                                                                                                                                                                                                                       211 FYLTDIAVVKIEDLELLAKNOPNLVSVKLTDC-EILDLVNFFKHASALEEFCGGTYNEEP
                                                                                                                                                                                                                                                                                                                                                                                                               211 ------EALKYIGAHCPELVTLNLQTCLQİTD-----BGLITICRGCHKLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99156230; PubMed=10048485;
Magage T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Miyajima Of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUUTT9; 034926;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fbox/LRR-repeat protein 7 (F-box and leucine-rich repeat protein 7).
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                        94;
LRR 7.
LRR 9.
LRR 10.
LRR 11.
LRR 12.
Missing (in isoform 2).
//FYId=VSP 008956.
L. > P (IN REF. 1; BAB28039).
H, C800E1861AF21BC3 CRC64;
                                                                                                                                                                                                                Length 436;
                                                                                                                                                                                                              5.5%; Score 175; DB 1; Length 436
22.2%; Pred. No. 5.1e-06;
Itive 47; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                      170 LLEQLNISWCDQV†KDGIQALVRGCGGLKALFLKGCTQLED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 LRRFALYLRRGGLTDVGLGYIGQYSPNVR 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 41-483 FROM N.A. MEDLINE=20003060; PubMed=10531035;
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48390 MW;
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436 AA;
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                                                                                                                                                                                                                                       Local Similarity
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272
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_TaxID=9606;
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETLNFYLTDIAVVKIEDLEL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 GLYTIAQCCPELR------RLEVSG--------CYNISNEAVFDVVSL-- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----IKLSPLHG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KQISIRY--LDMTD-CFVLE------DEGLHT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGRCCKRLKRLRIERGDDDGGMEDEEGTVSHRGLIALSQGCSELEYMAV----YVSDITN 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 GHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHV---LHALKLDKCSGFTTD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRPPHLESLKLKGKPRAAMFNLIPEDWG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAKNCPNLVSVKLTDCEILDLVNFFYGIASALEEFCGGTYNEEPERYSAISLPAKLCRL-G
                                  Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1e-05;
71; Mismatches 154; Indels 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4%; Score 172; DB 1; Length 491; 21.6%; Pred. No. 1e-05;
                                                                                                                                  (By similarity).
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 10 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARVCRRWYNL-----TIRLTG-
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EMBL; AB020647; BAA74863.2; ALT_INIT.
EMBL; AF174593; AAF04514.1; -.
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LERR 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; 1PR001810; F-box.
InterPro; 1PR007089; LRR cys.
InterPro; 1PR006553; LRR cys.
InterPro; 1PR006953; LRR cys.
InterPro; 1PR006945; SkpI_Skp2.
Pfam; PF00646; F-box; 1.
SWART; SW00256; PBOX; 1.
BROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:13604; FBXL7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ubl conjugation pathway;
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Matches 114;
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                      Pagano M.
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TISSUB-Brain;

K REDLINE=22388257; PubMed=12477932;

K Strausberg R.L.; Peingold E.A.; Grouse L.H., Derge J.G., Lechiler G.D., A Litschul S.E., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
102 ASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALYLR-RG--G 458
                                                   389 ITDHGVEYLAKNCTKLKSKIDIGKCPLVSDTGLECLALNCFNLKRLSLKSCESITGQGLQI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=20399565; PubMed=10945468; Ilyin G.P., Rialland M., Pigeon C., Guguen-Guillouzo C.; Ilyin G.P., Rialland M., Pigeon C., Guguen-Guillouzo C.; "cDNa cloning and expression analysis of new members of the mammalian
                                                                                                                                                             LIDVGLGYIGQYSPNVRWMLLGYVG-ESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
F-MAR-2004 (Rel. 43, Last annotation update)
F-box/LRR-repeat protein 2 (F-box and leucine-rich repeat protein (R-box protein FBL2) (F-box protein FBL2) (F-box protein FBL3).
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20003060; PubMed=10531035;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal
                                                                                                                                                                                                                                                                                                                               518 AATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVAINTNP 566
                                                                                                                                                                                                                                                                                                                                                                                                            449 VAANCFDLOTLNVQDCEVS-----VEALRF--VKRHCKRCVIEHTNP 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winston J.T., Koepp D.M., Zhu C., Elledge S.J., Harper J.W.; "A family of mammalian F-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 67:40-47(2000)
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ES-SILEKDGEWLHELALNNTVLETINFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDC- 242 139 SCVSITNSSLKGISEGCRN---LEYLNLSWCD--QITKDGIEALVRGCRGLKALLLRGCT 193 ----BILDLVNFFKHA------SALBEFCGGTYNEEPERYSAISLP--AKLC 282

194 QLEDEALKHIQNYCHELVSLNLQSCSRITDEGVVQICRGCH----RLQALCLSGCSNLT 283 RIGLTYIGKNELPIVEMFAAVLKKUDLLYAMLDTEDHCMLIQRCPNLEVLETRNV--IGD

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80 LRKLSLRGCIGVGDSSLKTFAQNCRNIEH-LNLNGCTKITDSTCYSLSRFCSKLKHLDLT 138

341 RGLEVIGRCCKRIKRIRIERGDDDQGMEDEEGTVSHRGLIALSQGCSELEYMAV-YVSDI

249 DASLTALGLN-

RGGL 459 381 RAGI 384

456

400 TNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALY----LR

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                                                                                                                                                                                                                                                         Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung, pancreas and placenta.
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
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-> W (IN REF. 5).
-> P (IN REF. 6).
BE6F824385121B4E CRC64;
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                                                                                                                                                             human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Ubl conjugation pathway; Leucine-rich
DOMAIN

5 5 F-BOX.
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EMBL; AF176518; AAF03128.1; ALT_INIT.
EMBL; AF186273; AAD56248.1; -.
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InterPro; IPR007089; LRR_cys.
InterPro; IPR006553; LRR_cys_sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK001438; BAA91691.1; -. EMBL; BC031556; AAH31556.1; -. EMBL; AL049953; CAB43222.1; -.
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Pfam; PF00560; LRR; 3.
SMART; SM00256; FBOX; 1.
SMART; SM00367; LRR_CC; 2
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126 LKSLHFRRMI-VKDSDLONLARDRGHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLE

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89;

5.4%; Score 170.5; DB 1; Length 423; 23.4%; Pred. No. 1.1e-05; Live 54; Mismatches 136; Indels 89;

Conservative

85;

Matches

Local Similarity

Query Match

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   Garzon A., Thode G.,
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Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Usery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Mismatches 145; Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.8%; Score 154; DB 1; Length 463; 20.5%; Pred. No. 0.00024;
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-1- SIMILARITY: Contains 8 leucine-rich (LRR) repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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GeneDB_SPombe; SPBC25B2.11; --
InterPro; IPR001810; F-box.
InterPro; IPR001611; IRR.
InterPro; IPR001699; IRR cys.
InterPro; IPR006553; IRR cys.
InterPro; IPR006553; IRR cys.
InterPro; IPR006551; IRR cys.
InterPro; IPR00650; IRR; ISRD.
SMART; SM00367; IRR; I.
PROSITE; PS50181; FBOX; I.
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DOMAIN 1 42 F-BOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Buffalo; TISUE=Liver;
X MEDLINE=99439713; PubMed=10508920;
X MEDLINE=99439713; PubMed=10508920;
X MEDLINE=99439713; PubMed=10508920;
X Ilyin G.P., Rialland M., Glaise D., Guquen-Guillouzo C.;
Iloentification of a novel Skp2-like mammalian protein containing
T "Identification of a novel Skp2-like mammalian protein containing
T F-box and leucine-rich repeats";
I FEBS Lett. 459:175-79(1999).
- I- FUNCTION: Probably recognizes and binds to some phosphorylated
- Proteins and promotes their ubiquitination and degradation.
- FUNCTION: Probably recognizes and binds to a SCF (SKPI-cullin-F-box)
- SUBCELLUIAR LOCATION: Cytoplasmic
- SUBCELLUIAR LOCATION: Cytoplasmic
- SUBCELLUIAR LOCATION: Cytoplasmic
- SINILARITY: Contains I F-box domain.
- SIMILARITY: Contains I F-box domain.
- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., INTERACTION WITH SKP1, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                476 WMLLGYVGE-SDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAATQLTSLRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
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23.0%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                             15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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InterPro, IPR001810, F-box.
InterPro, IPR007089; LRR Cys.
InterPro, IPR005553; LRR Cys.
                                                                                                                                                                                                                                                                                                                                                                          P-box/LRR-repeat protein 2-like
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PROSITE; PS50181; FBOX; 1.
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SMART; SM00256; FBOX;
SMART; SM00367; LRR CC
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Aspleton M., Jodin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J., Asha S.S., McZwan P.J., McKernan K.J., Malek J.A., Guptellano D.K., McKernan K.J., Malek J.A., Guptellano D.K., Holton B., Ketteman M., Madan A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Andreas R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M., Butkefley W.B., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra M.A., Schein J.E., Jones E.J.M., Marra
 288 YIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNV--IGDRGLEV 345
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Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
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Q8N531; Q9H5W9; Q9UKC7;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
F-box/LRR-repeat protein 6 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FBXL6 OR FBL6.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                             103 GVGDNALR---TFA-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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proteins and promotes their ubiquitination and degradation. SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---STGINRNSIPLQLPVEALQK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 141; DB 1; Length 53:
21.1%; Pred. No. 0.0029;
ive 52; Mismatches 162; Indels
                                                                                                                                                                                                                                                                   Note=No experimental evidence available, SIMILARITY: Contains 1 F-box domain. SIMILARITY: Contains 3 leucine-rich (LRR) repeats.
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Pfam; PF00560; LRR; 1.
SWART; SMO037; LRR CC; 3.
PROSITE; PS50181; PBOX; FALSE NEG.
UDl conjugation pathway; Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform 2). /FIId=VSP_008498.
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                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                      IsoId=Q8N531-2; Sequence=VSP_008498;
                                                                                                                                                                                                   lsoId=Q8N531-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-BOX.
LRR 1.
LRR 2.
LRR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC033066, AAH33066.1; -.
EMBL, AK026641; BAB15499.1; -.
EMBL, AF174592; AF04513.1; -.
Genew, HGNC.13603; FBKL6.
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Interpro; IPR001611; IRR.
Interpro; IPR00553; IRR cys su
Interpro; IPR008945; Skpl_Skpl.
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                                                                                                                         ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                   428 KEGSPFLTQKWCHTLRELDLSG-QGFSEKDLEQALAAFLSTPGGSHPALCSLNLRGTRVT 486
                                                                                                                                               389 -LD-----LRGCAR-----ITPAGLQDLPCRELEQ-----LHLGLYGTSDRLTLA 427
                                                                                       432 PLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLE 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes in VSG expression sites.
-!- DEVELOPMENTAL STAGE: Expressed only in the bloodstream form of the
                                                                                                                                                                                                                 -----BAKGCPSLOKLEMRGCLFFSERAL--AVAATQLT-----SLRYLWVQGYGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma equiperdum.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: May interact with adenylate cyclase to regulate its
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PIR; S16358; BWUT8Q.
InterPro; IPR001611; LRR.
InterPro; IPR001611; Znf ring.
Pfam; PF00067; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
PROSITE; PS50089; ZF RING 2; 1.
PROSITE; PS50089; ZF RING 2; 1.
PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91293076; PubMed=2065652;
Ross D.T., Raibaud A., Florent I.C., Sather S., Gross M.K.,
Storm D.R., Bisen H.;
346 G----RG-VAPGPGFPSLEELCLASSTCNFVSNEVLGRLIHGSPNLRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 RING-type zinc finger.
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01-MAY-1992 (Rel. 22, Last sequence update)
08-EBB-2013 (Rel. 41, Last annotation update)
Putative adenylate cyclase regulatory protein
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ARG/LYS-RICH (
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LIRR 5.
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EMBO J. 10:2047-2053(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FKHASALBEF------CGGTYNEEPERYSALSLPAKLCRLGLTYIGKNEL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 PIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 LVCFDGLQDLMNLEVLY-LRDVKSF-----TNVGAIKNLSKOMRELDLSG--CERIT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 RIRIERGDDDQCMEDEEGTVSHRGLIALS-QCCSEL-----EYMAVYVSDITN-- 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVR------WMLLGYVGESDAGLLB 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- ANLKE 569
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01-NOV-1991 (Rel. 20, Last sequence update)
03-Rel. 30, Last annotation update)
Putative adenylate cyclase regulatory protein (Leucine repeat protein)
(VSG expression site-associated protein F14.9).
                                                                                                                                                                                                                                                                                                                                                                       219 ITKG----FDKICALPQLTSLSICQTNVTDKDLRCIHP----DGKLKVLRYSSCHEITDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 VSNCKNFKDINGLERIVNLDKINLSGCHGV-----SSLGFVANLSNLKELDISGCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smiley B.L., Stadnyk A.W., Myler P.J., Stuart K.; The trypanosome leucine repeat gene in the variant surface glycoprotein expression site encodes a putative metal-binding domain and a region resembling protein-binding domains of yeast, Drosophila, and mammalian proteins.; Mol. Cell. Biol. 10:6436-6444(1990).
                                                                                                                                                                                                                                         ---SDLONLARDRGHVLHALKLDKCSG
                                                                                                                                                                                                                                                                                    161 LRKLRMKRTMVNDMWCSSIGLLKFLVHLBVDGSRGVTDITGLCRLK--TLBALSLDSCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AVV----KIEDLEL-----LAKNC--PNLVSVKLTDCEIL------DLVNF----
                                                                                                                                                                                                                                                                                                                                      163 FTTDGLFHIGRFC--KSLRVLFLEESSILEKDGEWLHELALNNTVLETLNF----YLTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei brucei.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                         Gaps
                                                                                                                                            Score 139; DB 1; Length 630;
Pred. No. 0.0052;
67; Mismatches 157; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLIGCEEI-----TPIGVVG----NLRNLKCLSTCWC----
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                                                                                                                                          DB 1; Length 630;
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                                                                                            69989 MW; F882E49A6A6E6651 CRC64;
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LRR 7.
LRR 8.
LRR 9.
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MEDLINE=91061751; PubMed=2247064;
                                                                                                                                                 4.48;
                                                                                                                                                                        20.9%;
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                                                                                                                                                                                              Matches 110; Conservative
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                                                                                               630 AA;
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460
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P23799;
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29;

Gaps

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383 LVCFDGLQDLNNLEVLY-LRDVKSF-----THVGAIKNLSKMRELDLSG--CERIT 430
                                                                                                                                                                                                                                                                                                                                                                           431 SL------SGLETLKGLEELSLEGCGEIMSFDPIWSLYHLRVLYVSECGNLE 476
                                                                                                                                                    161 LRKLRMKRTMVNDMWCSSIGLLKFLVHLEVDGSRGVTDITGLFRLK--TLEALSLDNCIN 218
                                                                                                                                                                                       219 ITKG----FDKICALPQLISISLCQTNVTDKDLRCIHP----DGKLKMLDISSCHRITDL 270
                                                                                                                                                                                                                     217 AVV----KIEDLEL-----LAKNC--PNLVSVKLTDCEIL------DLVNF---- 250
                                                                                                                                                                                                                                                                                      331 VSNCKNFKDLNGLERLVNLEKLNLSGCHGV-----SSLGFVANLSNLKELDISGCES 382
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                                                                                                                                                                          163 FTTDGLFHIGRFC--KSLRVLFLEESSILEKDGEWLHELALNNTVLETLNF----YLTDI 216
                                                                                                                                                                                                                                                                -----FKHASALEEF------CGGTYNEEPERYSAISLPAKLCRLGLTYIGKNEL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                            - LRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVR------WMLLGYVGESDAGLLE
                                                                                                                                126 LKSLHFRRMIVKD------SDLONLARDRGHVLHALKLDKCSG
                                                                                                                                                                                                                                                                                                                                                      355 RLRIBRGDDDQGMEDEEGTVSHRGLIALS-QGCSEL------EYMAVYVSDITN--
                                                                                                                                                                                                                                                                                                                                                                                                                477 DLSGLQCLTGLEEMYLHGCRKCTNFGPIWNLRNYCVLELSCCENLDDLSGLQCLTGLEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=90236305; PubMed=2158927; Melnick L., Sherman \mathbb{R}.; "Nucleotide sequence of the COR region: a cluster of six genes in the
                                                                                                                                                                                                                                    ---LKNLCDFRLVLLDHEEKITDLPLDNGVRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales, Saccharomycetaceae, Saccharomycetales
                                                                                                , Pred. No. 0.015;
69; Mismatches 156; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 FA--KGCPSLOKLEMRGCLFFSERALAVAATQLTSLRYL-WVQGYG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 IGGLERLVNIEKLDLSGCCGLSSSVF----MELMSLPKLQWFYGFG 611
                                                                                    4.2%; Score 133; DB 1; Length 630; 20.7%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TTIĠVVĠ----NLRNLKCLSTCWC---
                       6
511 C -> L (IN REF. 2).
522 D -> E (IN REF. 2).
546 EITT -> KLQP (IN REF. 2).
549 V -> I (IN REF. 2).
582 L -> V (IN REF. 2).
620 K -> E (IN REF. 2).
620 K -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
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SEQUENCE FROM N.A.
MEDLINE=87064430; PubMed=3023893;
Perozzi G., Prakaeh S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||:::
537 YLIGCEEI-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA repair protein RAD7. RAD7 OR YJR052W OR J1665.
                                                                                                              Matches 109; Conservative
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ID RAD7_YEAST
AC P06779;
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                                                                                 늉
    MEDLINE=91081317; PubMed=2259625;
Lips S., Revelard P., Pays E.;
"A gene from the VSG expression site of Trypanosoma brucei encodes a protein with both leucine-rich repeats and a putative zinc finger.";
Nuclaic Acids Res. 18:7299-7303(1990).
-i- FUNCTION: May interact with adenylate cyclase to regulate its
                                                                               -!- FUNCTION: May be involved in the postranscriptional regulation
                                                                                          genes in VSG expression sites. DEVELOPMENTAL STAGE: Expressed only in the bloodstream form of the parasite.
                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; Zinc-finger;
                                                                                                                             -!- SIMILARĪTY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 23 leucine-rich (LRR) repeats.
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EMBL; X55978; CAA39448.1; -.
PIR; A36359; A36359.
PIR; S13724; S13724.
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PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
Repeat; Leucine-rich repeat; CA
DNA-binding.
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InterPro; IPR001841; Znf_ring.
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Pfam; PF00097; zf-C3HC4; 1.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 ISLPAKLCRIGITYIGKNELPIVFMFAAVLKKLDLL--YAML-----DTEDHCMLIQRCP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 KSLSNLLINCGSTLVSLG-----LSRLDSISNYALLPQYLVNDEFHSLCIEYPF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 NLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALSQGCS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 NEEDVNDEIII-----NLGQIGRILRKLVL-----NGCIDLIDSMINGLIAFIPEKC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELLAKNCPNLVSVKLTDCEILD---LVN-----PFKHASALEBFCGGTYNEEPERYSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 ----DESSKLVFNKLRDVLGGVSTANLNNLAKALSKNRALNDHTLQL-----
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                                                                                                                                              Yeast 10:811-818(1994).
-!- FUNCTION: This protein is one of 10 proteins (RAD1, 2,3,4,7,10,14, 16,22 and MMS19) involved in excision repair of DNA damaged with UV light, bulky adducts, or cross-linking agents.
-!- MISCELLANBOUG: Muchants with mutations in the RAD7, RAD14, RAD16, and RAD23 genes show partial incision defectiveness.
                                                                                         MEDIJINE-95066383; PubMed-7975898;
Huang M.-E., Manus V., Chuat J.-C., Galibert F.;
"Revised nucleotide sequence of the COR region of yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Mismatches 188; Indels 114; Gaps
"RAD7 gene of Saccharomyces cerevisiae: transcripts, nucleotide sequence analysis, and functional relationship between the RAD7 and RAD23 gene products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0000113; C:nucleotide excision repair factor 4 complex; IDA.
GO:000108; C:repairosome; IDA.
GO:0003677; F:DNA binding; IDA.
GO:0008094; F:DNA dependent ATPase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 132; DB 1; Length
23.1%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 279 LL -> FV (IN REF. 1).
504 505 AC -> RP (IN REF. 1).
565 AA; 63777 MW; 85C77357DC99737A CRC64;
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                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                           RAD23 gene products.";
Mol. Cell. Biol. 6:1497-1507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003677; F:DNA binding;
GO; GO:0008094; F:DNA depender
InterPro; IPR007089; LRR_cys.
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EMBL; L26347; AAA62860.1; -.
EMBL; L36344; AAA88755.1; -.
EMBL; Z49552; CAA89580.1; -.
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GermOnline; 141885; -.
SGD; SO003813; RAD7.
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MEDINE-ZERRECH, PubMed=1247932;

MEDINE-ZERRECH, PubMed=1247932;

MEDINE-ZERRECH, PubMed=1247932;

MICHINE-ZERRECH, PubMed=1247932;

MICHINE-ZERRECH, PubMed=1247932;

MICHINE-ZERRECH, PubMed=1247932;

MICHINE-ZERRECH, Mang L., Schaefer C.R., Blat N.K.,

MICHINER, Marusina R., Farmer A.A., Rubin G.M., Holp L.,

MICHINER, Marusina R., Romaldo M.F., Carninci P., Prange C.,

MICHINER, M., Modin T.B., Toohiyuki S., Carninci P., Prange C.,

MICHINER, M., Modernan K.J., Marlek J.A., Guaratane P.H.,

MARA S.S., Moderan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

MILIALON D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milialon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Militing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan J.W., Schwutz J., Myers R.M.,

Redriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butkerfield Y.S.N., Krzywinski M.I., Skalalus D.E.,

Miching M., Schein J.E., Jones S.J.M., Marra M.A.,

Roberzation and initial analysis of more than 15,000 full-length
                                                                      427 PLEVLSLEESDO!TTDSLSYFFSKVELNNLIECSFRRCLOLGDMAITELLL-NGARDSLR 485
                                                                                                                                                          443 GCDKLRRFALYLRRGGLTDVGL-GYIGQYSPNVRWMLLGYVGESDAGLLE-FAKGCPSLQ 500
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388 ELEYMAVYVSD-ITNASLEHI--GTHLKNL--CDFRLVLLDHEEKITDLPLDNGVRALLR
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Lora J.M., Geddes B.J., Briskin M., Distefano P.S., Bertin J.;
"PYPAF7, a novel PYRIN-containing Apail-like protein that regulates
activation of NF-kappa B and caspase-1-dependent cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NACHT, LER and PyD-containing protein 12 (PYRIN-containing APAFI-like protein 7) (Monarch-1).
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-1- FUNCTION: May mediate activation of CASP1 via ASC and promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1061 AA.
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MEDLINE=22162427; PubMed=12019269;
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944 RELDLSFNDLGDWGLWLLAEGLQHPACRLOKLWLDSCGLTAKACENLYFTLGINQTLTDL 1003
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                                      TVLETLNFYLTDIAV--VKIEDLELLAKNCPNLVSVKLTDCEILDLVNFFKHASALEEFC 261
                                                                                                                                                                  713 PNLIELSLYRNALGSRGVKLLCQGLRHPNC-KLQNLRLKRCRI------SSSACEDLS 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96437976; PubMed=8840504;
Huang M. B., Manus V., Chuat J.-C., Galibert F.;
"Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open
reading frames and a gene cluster with a counterpart on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 FFSERALAVAATQL----TSLRYLWVQGYGVSPSGRDLLV---MARPFWNI
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Ubiquitin ligase complex F-box protein GRR1.
GRR1 OR COT2 OR CAT80 OR YIRO90C OR 11885.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungl; Ascomycota; Saccharomycotina; Saccha Saccharomycetales; Saccharomycetales; Saccharomycetales.
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01-MAR-1992 (Rel. 21, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update
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MEDLINE=92017785; PubMed=1922034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                      Name=2; Synonyms=11;

IsoId=P59046-2; Sequence=VSP_005524;

Name=3; Synonyms=III;

IsoId=P59046-3; Sequence=VSP_005523;

TISSUE SPECIFICITY: Detected only in peripheral blood leukocytes,

predominantly in eosinophils and granulocytes, and at lower levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00161; IER.
InterPro; IPR00161; IER. RNinh.
InterPro; IPR00191; IER. RNinh.
InterPro; IPR00191; IER. RNinh.
InterPro; IPR00111; NACHT NTPASe.
InterPro; IPR00101; NACHT NTPASe.
InterPro; IPR004020; PAAD_DAPIN_dom.
Pfam; PF002158; PAAD_DAPIN; 1.
PR051TE; PS050837; NACHT, 11.
PR051TE; PS50837; NACHT, 1.
PR051TE; PS50837; NACHT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 131.5; DB 1; Length
; Pred. No. 0.04;
80; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP 005524.
L -> LR (IN REF. 3).
W, 8C10AFE4907C131B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 DAPIN domain.
SIMILARITY: Contains 1 NACHT domain.
SIMILARITY: Contains 8 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (In isoform 2). P 005524.
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                        SUBGNIT: Binds to ASC with its DAPIN domain.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
ALTERNATIVE PRODUCTS:
Name=1, Synonyms=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               567 INEETRSHLEKSLCWKVS-----PHIKMDLLQ-
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                                                                                                                                                                                              IsoId=P59046-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LER 2.
LER 3.
LER 5.
LER 5.
LER 7.
LER 7.
ATP (POTEN MISSING (1)
      activation of NF-kappa-B vía IKK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ММ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY15446; AAM18227.1; --
EMBL; AY154467; AAO18163.1; --
EMBL; AY116204; AAM75142.1; --
EMBL; AY116205; AAM75143.1; --
EMBL; AY116206; AAM75144.1; --
EMBL; BC028069; AAH28069.1; --
Genew; HGNC:22938; NALP12.
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Best Local Similarity 19.6'
Matches 117; Conservative
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265 YNEEPERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCM--L 322
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--GDYMHDTELNYF 410
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                                                       205 VLETLNFYLTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILDLVNFFKHASALEEFCGGT
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
F-box/LRR-repeat protein 4 (F-box and leucine-rich repeat protein 4)
FBX14 OR FBL4 OR FBL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20003060, PubMed=10531035;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION. MEDIJNB=20003061; PubMed=10531037; Winston J.T., Koepp D.M., Zhu C., Elledge S.J., Harper J.W.; "A family of mammalian F-box proteins.";
                                                                                                           --GCKNL----ERLTLV-FCKHITSV---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=20399565; PubMed=10945468;
Ilyin G.P., Rialland M., Pigeon C., Guguen-Guillouzo C.;
"cDNA cloning and expression analysis of new members of F-box protein family.";
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      -----LRTMKLT----SEETVFNYRLMIKRLNFSFV----
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MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ARDRGHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : | : | 270 DTTESSDLKEGLQDLSRXSRQFINNVLSNPSNQNICTSVT----RRSPVFALNMLPSEI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 -HLESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 LHLILDKLNQKYDIVKFLTVSKLWA-----Éİ----IVKILYYRPHÍNKKSQLDLF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 MRLRALETENMEIRNIRLAL--KILTIIEEYKKSLYAYCHSKLRGQQVENPTDNFIIWINSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IDDPKDRDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
            induces glucose repression. Is not an essential protein. Involved in substrate recognition in ubiquitin-dependent degradation.
                                                                      PATHWAY: Necessary for the glucose repression pathway. SUBUNIT: Part of a SCF B3 ubiquitin ligase complex containing SCBID. CS53, HATI and GRAI. SUBCELULAR LOCATION: Associated with the particulate fraction. Probably forms a complex by protein-protein interactions via its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 ----SQVCRRWYELDSLTRKHVTIAL------CYTTTPARLRRRFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0000142; C:contractile ring (sensu Saccharomyces); IDA. GO; GO:0005737; C:cytoplasm; IDA. GO; GO:000534; C:ncytoplasm; IDA. GO; GO:0005634; C:ncytoples; IDA. InterPro; IPR001810; F-box. InterPro; IPR001811; IRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151 AA; 132733 MW; 6BB6C46611E6F825 CRC64;
                                                                                                                                                                                                                                            -!- INDUCTION: Expressed constitutively at low levels. -!- SIMILARITY: Contains 1 F-box domain. -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS50181; FBOX; 1.
Glucose metabolism; Ubl conjugation pathway; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSLRSNMTEERNVRKTRVVDVVLDCVIPY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR 12.
POLY-ASN.
ASN-RICH.
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LER 3.
LER 3.
LER 4.
LER 5.
LER 6.
LER 7.
LER 9.
LER 9.
LER 10.
LER 10.
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EMBL; Z49590; CAA89617.1; --
EMBL; L47993; AAB39313.1; --
EMBL; A41529; AA1529.
GermOnline; 141922; --
SGD; S0003850; GRR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR007089; LRR_CYB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; 1.-
Pfam; PF00560; LRR; 1.
                                                                                                                                                                                                                         leucine-rich segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucine-rich repeat.
DOMAIN 314 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Schevtenko Y., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leucine-rich repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          numman and mouse curn experience.

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-1- SUBUNIT: Part of a SCF (SKPI-cullin-F-box) protein ligase complex (By similarity).

-1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

-1- TISSUE SPECIFICITY: Expressed in heart, kidney, liver, lung, pancrea, and placenta, but not in skeletal muscle.

-1- SIMILARITY: Contains 1 F-box domain.

-1- SIMILARITY: Contains 8 leucine-rich (IRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 126.5; DB 1; Length 621; 21.4%; Pred. No. 0.047; tive 65; Mismatches 161; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> G (IN REF. 1).
-> A (IN REF. 1).
D8FD51A5C4F922D3 CRC64;
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LIRR 3.
LIRR 4.
LIRR 5.
LIRR 6.
LIRR 7.
LIRR 8.
LIRR 8.
F -> Y
S -> G
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DOMAIN 277 332 F-BC
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SMART; SM00256; F-box; 1.
SMART; SM00367; LRR CC; 1.
PROSITE; PS50181; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:13601; FBXL4.
MIM; 605654; -.
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232
621 AA;
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Best Local S
Matches 98
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121 QYFDCLKSLHFR----RMIVKDSDLQNLARDRGHVLHALKLDKCSGFTTDGLFHIGRFCK 176

Conservative

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Similarity 98;

Gaps

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L-----KLDLLYAMLDTED 318
                                                                                                                                                                                                                                                   -----IEDDAYAEKDGCGMDSLNKKFSSAVLGEGPNNGYFDKLPYELIQLILNHLTLPD 299
                                                                                                                  391
                                                                                                                                       319 HCM--LIQRCPNLEVLETRNV--IGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTV 374
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SLRVLFLEESSILEKDGEWLHEL------ALNNTVLETLNFYLTDIAV--VKIED 223
                                                            375 SHRGLIALSQGCSELEYMA----VYVSDITWASLEHIGTHLKNLCDFRLVLLDHEBKITD
                                                                                                                                                                                                                                    431 IPIDNGVRALLRGCDXLRRFALYLRRGGLTDVGLGY------IGQYSPNVRWM
                                             LELLAKNCPNLVSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPERYSAISLP---AK
                                                                                                                                                                -----TKV
                                                                                                                                                                                                            ---RILDLWRCKNIT-
                                                                                                                                                               392 -CLEVISEMCPNLOALNLSSCDKLPPQAFNHIAKLCS-LKRLVLYR----
                                                                                                                                                                                                       478 LL-GYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERAL 515
                                                                                                                                                                                                                                                                                                 539 FLTANRSVCDTDIDELACNCTRLQQLDILGTRMVSPASL 577
                                                                           LCRIMOTC
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Title: Perfect score: Sequence:

US-10-009-791-22 3180 1 TKTSAPFLFTLSLRSNWTEE......QRSDFPDTVVPLDTATCVDT 606 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	LRR-containing F-b	hypothetical prote	transport inhibito	F13K23.7 protein -	hypothetical prote		hypothetical prote	protein F20N2,2 [i	probable glucose r	hypothetical prote	unknown protein T2	hypothetical prote		~		hypothetical prote	probable regulator	hypothetical prote	hypothetical prote	hypothetical prote	F	hypothetical prote		hypothetical prote	regulatory protein	ESAG 8 protein - T	prot	hypothetical prote	disease resistance
SUMMARIES	a a	T52139	E85040	T48087	F86261	T09902	T48193	C71419	E96598	A84649	S44609	G96837	T08604	D96512	T41312	T45861	B84547	T39987	T43444	B84856	B85072	T52349	F86291	A96799	B86347	BWUT8Q	S13724	T05201	7143	D85188
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	Score	2126.5	818	812.5	749.5	693	229.5	209.5	188	187.5	186	176.5	176.5	172.5	169.5	168.5	159.5	154	152	149.5	148	147.5	147.5	146	140	139	139	135.5	134.5	134.5
	Result No.		7	٣	4	ιΩ	ø	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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254 ASALBERCGGTYNEE---PERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKLDLL 310

VSG expression sit	RAD7 protein - yea	hypothetical prote	disease resistance	GRR1 protein - yea	hypothetical prote	hypothetical prote	N7-like protein (i	hypothetical prote	internalin protein	probable disease r	hypothetical prote	hypothetical prote	F6D8.13 [imported]	disease resistance	hypothetical prote
A36359	A25226	E85358	T52348	A41529	T04426	T23945	A85069	T08680	AF1116	H84513	T33367	E96838	D96567	T52346	H96695
7	N	0	~	N	~	N	0	7	7	~	~	C4	N	N	N
630	565	301	1217	1151	1405	551	307	250	1778	1215	556	578	465	1189	419
4.2	4.2	4.1	4.1	4.0	4.0	4.0	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.8
133	132	131.5	131.5	127.5	126.5	126	125	124.5	122.5	122	121.5	121.5	121	120.5	119.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 T52139 ILRR-containing F-box protein [imported] - Arabidopsis thaliana NAILernate names: hypothetical protein At2393940 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Deresion: 152139; C94823 R;Xie, D.X.; Feys, B.F.; James, S.; Nieto-Rostro, M.; Turner, J.G. Science 280, 1091-1034, 1999 A;Title: COII: An Arabidopsis gene required for jasmonate-regulated defense and fertili A;Reference number: 225980; MUID:98248619; PMID:9582125 A;Accession: T52139 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ A;Status: preliminary: translated from GB/EMBL/DDBJ A;Stell: Scyons reference: BMBL:AF036340; PIDN:AAC17498.1 A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Reference number: A; Rounaley, S.D.; Eisen, J.A.; Salzberg, S.D.; Fraser, C.M.; Venter, Nature 402, 751-768, 1999 A;Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference: A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Residuse: 1-592 AXIB- A;Residuse: A;Residus		QY 74 TTTPARLRRRPPHLESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRR 133	Qy 134 MIVKDSDLQNLARDRGHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDG 193
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and is
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362 FVSKGCRKLESVLYFCVQFTNAALFTIARKRPNLKCFRLCVIEFFAPDYKTNEPLDKGFK 421
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A)Cross-references: EMBL:AL163816
A)Experimental source: cultivar Columbia; BAC clone T20010
A)Experimental source: cultivar Columbia; BAC clone T20010
B)Ruegger, M; Dewey, E; Gray, B; Hobbie, L; Turner, J; Estelle, M.
B)Ruegger, M; Dewey, E; Gray, B, Hobbie, L; Turner, J; Estelle, M.
A)Describtion: The TIRI protein of Arabidopsis functions in auxin response: A; Reference number: Z25881
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250;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A, Status: preliminary
A, Molecule type: DNA
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A; Introns: 156/2;
A; Note: T20010.80
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Best Local S
Matches 201
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                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AT4903190 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 (Specession: B88040 #spanonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col. Nature 402, 769-777, 1999 #iftle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-585 <STO>
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C;Genetics:
A;Gene: AT4g03190
A;Map position: 4
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R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, Submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16896

A;Accession: T09902
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359 VGLVAISAGCPKLHSILYFCKQMTNAALIAVAKNCPNFIRFRLCILEPHKPDHITFQSLD 418
                                  NGVRALLRGCDKLRRFALYLRRGGITDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAK 494
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 KKLIRTNRFVSLERLHRLMVRAPQLTSLGTGSFSPDNVPQGEQQPDYAAAFRACKSIVCLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 RWYELDSLIRKHVTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNLIPEDWGGHVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 VSVKLTD-CEILDLVNFFXHASALEEFCGGTYN-----EEPERYSAISLPAK--LCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 VLGRCCKRLKRLRIBRGDDDGGMEDBEGTVSHRGLIALSQGCSELEYMAVYVSDITNASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 AVAATCKELRELRIFPFDP---REDSEGPVSGVGLQAISEGCRKLESILYFCQNMTNGAV
                                                       GCPSLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHVLHALKLDKCSGFTTDGLFHIGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TKTSAPFLFTLSLRSNMTBERNVRKT-----RVVDVVLDCVIPYIDDPKDRDAVSQVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Realdudes: 1-614 <BEV.
A;Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.220
A;Experimental source: cultivar Columbia; BAC clone T22A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614;
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21.8%; Score 693; DB 2; Length 61
Best Local Similarity 30.7%; Pred. No. 2.6e-46;
Matches 190; Conservative 108; Mismatches 277; Indels
                                                                                                                                                                          555 IPSRK--VATNTNPDETVVVEHPAHILAYYSLAGQRSDFPDTV 595
                                                                                                                                                                                             | : | | | | | | | | INBURINGMEQNEEDEREKVD---KLYLYRTVVGTRKDAPPYV 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 192/2; 358/3
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Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roonley, L.; Sakano, H.
A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; MuID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 YENEPDPESFAKIMTAIKKYTSLRSLSGFLEVAPLCLPAFYPICQNLISLNLSYAAEIQG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHCM-LIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSH 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHLIKLIQLCKRLQRLWILDSIGDKGLAVVAATCKELQELRV-FPSDVHGEEDNNASVTE 358
                                                                                                                                                               561
                                                                                                                369 MGCPKLESVLYFCRQMTNAALITIARNRPNMTRFRLCIIEPKAPDYLTLEPLDIGFGAIV 428
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                       F13K23.7 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFACLKGETNVAA----LERLVARSPNLKSLKLNRAVPLDALARLMSCAPQLVDLGVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVVLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFYL----TDIAVVKIEDLELLAKNCPNLVSVKLTDCEILD-LVNFFKHASALBEFCGGT
                                                                                                                                                             LEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVA
                          QCCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHE--EKITDLPLDNGVRALL
                                                                                             RGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLOK
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                                                                                                                                                                                                                                 562 INTNPDETVVVEHPAHILAYYSLAGQRSDFPDTVVPLD 599
                                                                                                                                                                                                                                                     ; Score 749.5; DB 2;
; Pred. No. 8.8e-51;
97; Mismatches 258;
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33.8%;
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Best Local Similarity
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A; Residues: 1-577 <STO>
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hypotherical protein - Arabidopsis thaliana
C;gecies: Arabidopsis thaliana (mouse-ear cress)
C;baces: Olumbia
C;bacession: C71419
C;bate: O3-Ang-1998 #sequence_revision O3-Aug-1998 #text_change O5-Dec-1998
C;bate: O3-Ang-1998 #sequence_revision O3-Aug-1998 #text_change O5-Dec-1998
C;bacession: C71419
C;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Di; R;Bevan, M.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Terryn, N.; Gie avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomene erhabets N.
C; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis the A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-712 cBEV>
A;Cross-references: GB:297339; NID:92244901; PID:9226930; PID:92244904
C;Genetics:
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, B16-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, X.; Liu, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. P.; Southwick, A.M.; Sun, H.; Tallon, A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 PNVRWMLIG----YVGESDAGLLEFAKGCPSLOKLEMRGCLFFSER---ALAVAATQITSL 525
447 QDITDKSLVSLSK-CSLLQTFESRGCPNITSQGLAAIAVRCKRLAKVDLK---KCPSIND 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584 ALLYCQRIGNSALQEIGKGYLKAGTFDHKFQNIGDMPLAELGEGCPMLKDLVLSHCHHI 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein F20N2.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 KKLKDLTLSDCYFV--SCKGLEAIAHGCKELERVEINGCHNIGTRGIBAIGKSCPRLKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 CMLIQRCPNLEVLETRN-VIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467 LIAVAQGCHRLKNIKLKLQCVSVTDVAFAAVGELCTSLERLALYSFQ-HFTDKGMRAIGKGS
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                                                                                                            527
                                                                                         503 AGLLALAHFSQNLKQI------NVSDTAVTE
                                                           --LLVMARPFWNIELIPSRKVATNTNPDETVVVE
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Best Local S:
Matches 83,
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                                                                                                                                                                                                                                                                                                                                                                                                                                В.
                                                                                                                                                                                                                                                                                                                hypothetical protein F7A7.240 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (S. Accession: T48193 (S. Baysenact, C.; Dasseville, R.; De Clerck, B. Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, submitted to the Protein Sequence Database, March 2000 A; Reference number: 224487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 GE-SDAGLLEFAKGCPSLOKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRD 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 KMYKQKLDASSCQNLTHRGLT-----SLLSGAGYLQRLDLSHCSS---VISLDFASS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LRSDYLPRILTRYRNÍTDĽDLÍFCPRVTDYALSVVGCLSGPTĽRŠĽDĽSRSGSFSAAĞLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAAM--FULIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHVLHA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ILKLOHLEELLLEGCFGVDDDSLKSLR-HDCKSL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 DLVNFFKHASALEEFC--GGTYNEEPERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 LKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ESSILEK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | : | | : | | : | | : | | KVYKQIRVLKPFDLLSEELVFIILDLISP---NPSDLKSFSLTCKSFYQLESKHRGSLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----MRDADAAVVAEARS--LER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 DGEWIHELALNNTVLETINFYLTDIAVVKIEDL-ELLAKNC-----PNLVSVKLTDCEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ELTRKHVTIALCYTTTPARLRRF------BHLESLKLK------GKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 RNVRKTRV------VDVVLDCVIPYIDDPKDRDAVSQVCRRWYBLDS-----
                                        TOLISLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVAININPDETVVVEHPAHIL
                                                                         540 HRYSNMRFVWLSSCLISRGGCRGVSHALPNVVVEVFG----ADGDDDEDTVTGDYVETLY
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A;Introns: 213/3; 255/3; 259/3; 294/3; 350/1; 376/1; 419/2; 517/3; 601/3
A;Note: F7A7.240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 229.5; DB 2; Length 618; larity 23.5%; Pred. No. 6.6e-10; Conservative 86; Mismatches 210; Indels 189.
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                                                                                                                                                                                                   596 LYRSLDGPRKDAPKFVTIL 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 KLALKCVNLVEIDLSNATE--
                                                                                                                                                  580 AYYSLAGORSDFPDTVVPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-618 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T48193
A;Status: preliminary
A;Molecule type: DNA
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Matches 149;
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-VLETRNVIGDRGLEVLGRCCKRLKRLRIERGD--DDQGMEDEEGTVSHRGLIALSQGCS 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apportational protein C02FS.7 - Caenorhabditis elegans
N;Contains: hypothetical protein C30AS.1
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44609; S44774
R;Anderson, K.
A;Description: Sequence of the C. elegans cosmid C02FS.
                                                                                                                                                                                                                                                                                        -----EGCAQLEKLELNR
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                                                                                                                                                                                                                  220 KIEDLEL--LAKNCPNLVSVKL----TDCEILDLVNFFKHASALEFFCGGTYNEEPER
                                                                                                                                                                                                                                                                                                                                                           272 YSAISLPAKLCRIGITYIGKNELPIVFWFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLE-
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A,Cross-references: BRBL:110990; NID:g156211; PID:g156212
A,Experimental source: BRBL:110990; NID:g156211; PID:g156212
A,Experimental source: Cosmid C30A5
A,Note: designated as C30A5.1 protein
C,Genetics:
C,Genetics: 39/3; 67/2; 197/2; 264/3; 431/3
F,11-197/Product: hypothetical protein C30A5.1 #status predicted <CPR>
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5.8%; Score 186; DB 2; Length 489;
Best Local Similarity 21.9%; Pred. No. 1.2e-06;
Matches 108; Conservative 66; Mismatches 154; Indels 166;
                                                                         Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 LTLEACSRIGDEGLLAIARSCSKLKSVSIKNCPLVRDQGIAS----
                                                                      5.9%; Score 187.5; DB 2; Length 25.6%; Pred. No. 1.3e-06; ive 43; Mismatches 102; Indels
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A.Residues: 1-489 - .....
A.Gross-references: EMBL:L14745; NID:g289607; PID:g289614
A.Experimental source: cosmid C02F5
                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1993
A;Description: Sequence of the C. elegans cosmid C30AS.
A;Reference number: S44774
A;Accession: S44774
                                                                                                                                                                                                                                                                                                                                                                                                           213 CSTIT----DKGLVAIAKS------
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                                                Query Match
Best Local Similarity 25.6%
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A; Map position:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84649
R;Inn, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Atture 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 -ITWASLEHIGT------HLKNLCDFRLVLLDHEEKITDLPL------DNGVRAL- 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : :: : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTDIAVVKIEDLELLAKNCPNLVSVKLTDCEILDLVNFFKHASALEEFCGGTYNEEPERY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 SAISLPA-----KLCRLGLTYIGKNELPIVFMFAAVLKKL---------DLLYAM 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 SALLSPSPSFTLQSLSLVLDLISDRLIIAITGSLPQLVKLDLEDRPEKEPFPDNDLTYTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 LDTEDHCM-----LIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGM 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 VKEISQY-FDCLKSLHFRRMIVKDSDLQNLARDRGHV---LHALKLDKCSGFTTDGLFHI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIGLSSLTLNCLR-----LNAASVRGVLGPHLRELHLLRCSLLSSTVLTYI 111
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                                                                                                                                                A; Cross-references: GB: AE005173; NID: 98778504; PIDN: AAF79512.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LKRLDLENLCSVACVSTTLRSAVVSGVLPSLTSLDL----SVFS--PDDETLNHVLRG
                                                                                                                                                                                                                                                                                                                         5.9%; Score 188; DB 2; Length 607;
23.0%; Pred. No. 1.2e-06;
cive 74; Mismatches 185; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 EDEEG---TVSHRGLIALSQGCSELEYM----AVYVSD--
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.0%
Matches 132; Conservative
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A,Molecule type: DNA
A,Residues: 1-628 <STO>
                                                                                                                  1-607 <STO>
       A,Accession: E96598
A,Status: preliminary
A,Molecule type: DNA
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A;Gene: At2g25490
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A,Gene: F20N2.2
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Db 140 VLSLAVGCKKIRRIAHLIRCLANVASVEMLEYFGKLETLEELC 180 275 ISLPAKLCRIGITYIGKNEL	PUBLICATION TO THE CALL SOURCE TO THE CALL CHANGE 11-Jun-1999 C. Decides: ClyCine max (Soubsan) C. Species: ClyCine. C. Decides: ClyCine. R. Accession: T00604 R. Accession: T006
QY 13.7 KDSDLONLARDRGHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWL 196 16.3 TDASCENIGR-YCHKLNYINLENCSSITDRAMKYIGDGCPNLSYLNISWCDAIGDRGV-219 19.7 HELALNN-TVLETLINFYITDIAVVKIEDLELLAKOCPNLSYLNISWCDELIDLINFF 251 22.0 -QIILSWCKSLDTLIRGCEGLTENVFGSVEAHMGAIKKLNILQCFQLTDITVQNIAN-276 DD 25.2 KHASALEBFCGGTYNEEPERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKLDLLY 311 QY 27.7 -GATALEYLCMSNCNQISDRSLVSLG301 DD 27.7 -GATALEYLCMSNCNQISDRSLVSLG	SSULT 11 (6837 known prote: Species: Arr Species: Arr Accession: Theologis, Theologis, Theologis, Anthors: Hu A. i. Ro Accession: Title: Sequistrate Species: Arr A. i. No Accession: Title: Sequistrate Reference: Referenc

Db 302 AAIAEKCKRLRKLHIDGWKANLIGDEGLVAVAKFCSQLQELVLIGVNPTTLS 353 Qy 404 LEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCDKLRRFALYLRRGCLTDVG 463	C. Accession: T41312; T41480 C. C, Accession: T41312; T41480 R;Gwilliam, R.; Barrell, B.G.; Rajandream, M.A.; Wedler, H.; Wambutt, R. submitted to the EMBL Data Library, September 1998 A;Reference number: Z21987 A;Accession: T41312 A;Accession: T41312 A;Ratus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 1-563 <gmi>A;Residues: 21991 R;Bothe, G.; Pohl, T.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. R;Retence number: Z21997 A;Reterence number: Z21997 A;Reterence number: Z21997 A;Accession: T41480 A;Atatus: preliminary; translated from GB/EMBL/DDBJ A;Accession: T41480 A;Accession:</gmi></gmi></gmi></gmi></gmi></gmi></gmi></gmi></gmi></gmi></gmi></gmi>	A, Residues: 1-563 < BOTS A, Cross-references: EMBL:AL031644; PIDN:CAA21066.1; GSPDB:GN00068; SPDB:SPCC613.14 A, Experimental source: strain 972h-; cosmid c613 C; Genetics: C; Genetics: SPCC330.02; SPCC613.14 A, Map position: 3 A, introns: 19/3 Query Match Est Local Similarity 20.1%; Pred. No. 3e-05; Best Local Similarity 20.1%; Pred. No. 3e-05; Matches 109; Conservative 76; Mismatches 158; Indels 199; Gaps 23;	71 LCYTTTPARLERREPHLE		317 402 372 444 425
OY 350 CKRLKRLRIERGDDDQGMEDEEGTVSHRGLI-ALSQGGSELEYMAVYVSDITNASLEH 406 DD 302 CPNLRS:: : : : : : : : : : : : : : : : : : :	RESULT 13 D96512 hypothetical protein F2G19.16 [imported] - Arabidopsis thaliana C;Species Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66512 C;Accession: D66612 C;Accession: D66612 C;Accession: D66612 C;Accession: D66612 C;Accession: D66612	A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D96512 A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Crossiduse: 1-518 <sto> A;Crossiduse: 1-518 <sto> C;Genetics: A;Crossiduse: A;Crossiduse: BB:AE005173; NID:g11321778; PIDN:AAG34255.1; GSPDB:GN00141 C;Genetics: A;Genetics: A;Genetics: A;Genetics:</sto></sto>	Query Match S.4*; Score 172.5; DB 2; Length 518; Best Local Similarity 20.4*; Pred. No. 1.5e-05; Matches 107; Conservative 60; Mismatches 166; Indels 191; Gaps 20; Qy 30 DVVLDCVIPYIDDPRDDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPH 86	103 147 135 187	OY 247 LVNFFKHASALEEFC-GGTYNEEPERYSAISLPAKICKIGITYIGKNELPIVFMPAAVIK 305 DD 208ASSLKSICLKELYNGQC-FGPVIVGAKNIKSLKIFRC-SG 245 OY 306 KIDLLYAMLDTEDHCMLIORCPNLEVLETRNVIGDRGL 343 DD 246 DWDLLLQEMSGKDHGVEIHLERMQVSDVALSAISYCSSLESIHLVKTPECTNFGL 301 OY 344 EVLGRCCKRIKRLRIERGDDDQGMEDEGTVSHRGLIALSQGSELEYMAVYSDITNAS 403 OY 1 =

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Job time : 32 secs
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----SEVIDEALQYIVNFPLPMLKALDVSWIR 520
                                                                                                45 DRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLESLKLKGKPRAAMFNLI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 -----ILPFLPCIFNRFDSVTKLALRCDRRSFSLSDRALFIVSIRCSNLIR----- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHELALNNTVLETLNFYLT-DIAVVKIEDL-----ELLAKNCPNLVSVKLTDCEILDL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 UNFFKHASALEEFCGGTYNEEPERYSAISLPAKLCRLGLTYIGKNELPIVFMFAAVLKKL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 DLLYAMLDTEDHCMLIQRCPNLEVLETRNV--IGDRGLEVLGRCCKRLKRLRIERGDDDQ 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RMIVKDSDLQNLARDRGHVLH 153
                                                                   483 GESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GNW----DRVFEMNGNGNSSLTE-----IRLERLQVTDIG-----LFG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Residues: 1-522 <BAR>
A)Cross-references: EMBL:AL132978
A)Experimental source: cultivar Columbia; BAC clone F3A4
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 ALKLDKCSGFTTDGLFHIGRFCKSLRVL---
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                                                                                              | :| | : | |:|:|| | 521 GMNDKLVCDFESKKPTLEKL--
481 GHTLRTLDL-NGM--
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LI 558
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621	256.5	249.5	235	229.5	229	221	217	217	213	213	209.5	203	193.5	188	188	187.5	184	183.5	180	180	179	176.5	176.5	175	175	175	172.5	172.5
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ALIGNMENTS

1	004197 PRELIMINARY; PRT; 592 AA.	1997 (TrEMBLrel. 04,	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)	_		Arabidopsis thaliana (Mouse-ear cress).	Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	NCBI_TaxID=3702;	(1)	SEGUENCE FROM N.A. STRAIN=cv. Columbia;	um K.A., Lin X., Phillips C.A., 1	Fuhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,	Venter J.C.;	Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.		SEQUENCE FROM N.A.	STRAIN=CV COLUMDIA;	DOMESTICATED TO DOME OF M. M. M. M. M. M. M. M. M. M. M. M. M.	TATTOT		SEQUENCE FROM N.A.	STRAIN=Cv. Columbia;	MEDLINE=98248619; PubMed=9582125;		"CUII: an Arabidopsis gene required for jasmonate-regulated defense	and refutility griphip 280:1091-1094 (1998)		SEQUENCE FROM N.A.	Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Bann J.,	BOWSET L., CAININGI F., DAIE U.M., GIDBON H.A., GOLUBWILN A.D.,	
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Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.
Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Indels
                                                                                                                                                                                 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIELIPSRRVPEVNQQGEIREMEHPAHILAYYSLAGQRIDCPITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2126.5; DB 1 Pred. No. 6.6e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 407; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 VGELTXYEKVKPPPRLCFLGLTYMGTNEMPVIFPFSMKLKKLDLQYTFLTTEDHCQIIAK 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESLKLKGKPRAAMFNLIFEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 RCHVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EPERYSAISLPAKLCRIGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 CPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIBRGDDDQGMEDEEGTVSHRGLIALSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 CPNLLILEVRNVIGDRGLEVVGDTCKKLRRLRIERGDDDPGLQEEQGGVSQLGLTAVAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 CSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPLDNGVRALLRGCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 SCC-FSERALSLAVLOMPSLRYIWVOGYRASQTGLDLLLMARPFWNIEFTPPSPESFNHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 VPDEALHLVMGHVEDPRDREAASRVCRRWHRIDALTRKHVTVAFCYAARPARLRERFPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLRRFALYLRRGGLTDVGLGY1GQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQKLEMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                       "Oryza sativa nipponbare(GA3) genomic uma, circumstalore;P0529E05.";
clone:P0529E05.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003279; BAB84399.1; --
Gramene; QRMG4; --
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001810; F-box.
InterPro; IPR001611; LRR.
Pfam, PF00646; F-box, 1.
SEQUENCE 630 AA, 70619 MW, BFA12F8FIC93F23C CRC64;
                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%; Score 1855.5; DB 10 60.9%; Pred. No. 1.1e-149;
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    Created)
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Matches 352; Conservative
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                           01-MAR-2003 (TrEMBLr
P0529E05.15 protein.
P0529E05.15.
                                                                                                                       Oryza Bativa (Rice)
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m RESULT us-10-009-791-22.rspt

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STRAIN=cv. TGX1835-2E;
Christianeen L.C., Ulvskov P.;
"Putative Glycine max sbCO11 homologous to Arabidopsis COI (atFBL2).";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF536527; AAN31713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 DNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGOYSPNVRWMLLGYVGESDAGLLBFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 KGCPSLQKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 VSHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VSHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHEEKITDLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 DNGVRALLIRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGCPSLQKLEMRGCLFFSBRALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIE
                                                                                                                                                  Glycine max (Soybean).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae, Papilionoideae, Phaseoleae, Glycine.
NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 1200; DB 10; Length 237; 99.1%; Pred. No. 2.9e-94; Live 1; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 LIPSRKVATNTNPDETVVVEHPAHILAYYSLAGQRSDFPDTVVPLDTATCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 AA; 26280 MW; 6F8C6B17AF74E1FD CRC64;
           01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative coronatine-insensitive 1 (Fragment).
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Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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Q9C5Y7
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                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last an
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Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.6%; Score 1766.5; DB 10; Lengt Best Local Similarity 59.5%; Pred. No. 3.9e-142; Matches 344; Conservative 84; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Rice Genomic Sequence.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ACI35205, AAPO6838.1; -.
Hypothatical protein.
SEQUENCE 589 AA; 66265 MW; 24E53DB072804D34 CRC64;
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                                         PRELIMINARY;
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Thelander M., Fredrikeson D., Schouten J., Hoge H.C., Ronne H.;
Thelander M., Predrikeson D., Schouten J., Hoge H.C., Ronne H.;
"Cloning by pathway activation in yeast: identification of an
Arabidopsis thaliana P-box protein that turns on glucose repression.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ARS191816, ARK01147.1;
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                       Created)
PRT;
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                                                                                       01-JUN-2001 (TrEMBLrel. 17,
PRELIMINARY;
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Pfam; PF00560; LRR; 1.
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Matches 200;
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Q94AU0;
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01-MAR-2003 (
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Arabidopsis thaliana (Mouse-ear cress).
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"Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M.,
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez
Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedh
Mewes H.W., Lemcke K., Mayer K.F.X.,
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Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk K., Jones T., Kim C.J., Ngnyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC05275; AADJ4471;
EMBL; AL161496; CAB77804.1;
EMBL; AX150427; AAN12969.1;
the EMBL/GenBank/DDBJ databases
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SEQUENCE 585 AA; 65647 MW; D39D627C82864D83 CRC64;
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Last sequence update)
Last annotation update)
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Interpro; IPR001810; F-box.
Interpro; IPR001611; LRR.
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Pfam; PF00560; LRR; 1.
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                                                                                        PROUBENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,

Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,

Jang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninoi P., Chen H., Cheuk R.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.

Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,

Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,

Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,

Ecker J.R., Theologis A.,

"Full Length CDNA of gene AT4903190 (GI:7270189).",

Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.

R. InterPro; IPR001810; F-box.

R. InterPro; IPR001810; F-box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
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LKGKPHPADYNLVPDGMGGYAMPWIEAMAAKSSSLEEIRMKRIVVTDECLEKIAASFKD-
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           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                             Length 585;
homolog of transport inhibitor response 1 protein
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                                                                                                                                                                                                                                                                                                    65632 MW; 9479071377F72276 CRC64;
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Pred. No. 1.3e-60;
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Pfam; PF00560; LRR; 1.
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCL-ASEVSFSALERLVTRCPNLKSLKLNRAVPLEKLATLLQRAPQLEBLGTGGYTAEVR 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transport inhibitor response 1 (Putative transport inhibitor response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIRI OR T20010_80 OR AT3G62980.
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; edicotyledons; core eudicots; rosids;
NUBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 VLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLESLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 LKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu I., Davis R.W.,
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Obermaier B., Ottenwaelder B., Duchemin D., Zeitler K., Mewes
Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 594;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Ruegger M., Dewey E., Gray B., Hobbie L., Turner J., Estelle
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 104; Mismatches 250; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ecker J.R., Theologis A.; "Arabidopsis Open Reading Frame (ORF) Clones."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 AA; 66798 MW; 9E19ED5DABF40D07 CRC64;
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  594 AA
  PRT;
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EMBL, AF005047, AAB69175.1; --
EMBL, AL163816; CAB87743.1; --
EMBL, BT001946; AAN71945.1; --
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INTERPRO; IPR001810; F-box.
INTERPRO; IPR001611; IRR CYB.
INTERPRO; IPR007089; IRR CYB.
INTERPRO; IPR00945; SKpl_Skp2.
PRELIMINARY;
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Pfam; PF00560; LRR; 1.
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                                        311 CQCPKLQRLWVLDYIEDAGLEVLASTCKDLRELRV--PPSEPFVMEPNVALTEQGLVSVS 368
                                                                                                                       441
                                                                                                                                                          369 MGCPKLESVLYFCRQMINAALITIARNRPNMTRFRLCIIEPKAPDYLTLEPLDIGFGAIV 428
                                                                                                                                                                                                                                        501
                                                                                                                                                                                                                                                                                                 429 EHCKDLRRLSL---SGLLTDKVFEYIGTYAKKMEMLSVAFAGDSDLGMHVULSGCDSLRK 485
                                                                                                                                                                                                                                                                                                                                                             502 LEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVA 561
                                                                                                                                                                                                                                                                                                                                                                                                                     486 LEIRDCP-FGDKALLANASKIETMRSLWMSSCSVSFGACKLLGQKMPKINVEVIDERG-A 543
324 QRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRGLIALS
                                                                                                                 384 QGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLDHE--EKITDLPLDNGVRALL
                                                                                                                                                                                                                                        RGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQK
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SEQUENCE FROM N.A.
SEQUENCE A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kin C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridipantee; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 3. I. Se features of the regions of 4,504,864 bp covered by sixty Pl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.9%; Score 760.5; DB 10; Length 575; 33.6%; Pred. No. 3.9e-56; Indels 51; ive 96; Mismatches 246; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Ta
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Transport inhibitor response-like protein.
AT3G26830, MDJ14.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 INTNPDETVVVEHPAHILAYYSLAGORSDFPDTVVPLD 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 PDSRRPESCPV----ERVFIYRTVAGPRFDMPGFVWNMD 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20277480; PubMed=10819329;
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InterPro; IRR008945; Skpl_Skp2.
Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
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Matches 199; Conservative 9
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STRAIN=Columbia,
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DVVLDCVI PYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPHLES

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209
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DTEDHCM-LIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 IHGSHLIKLIQHCKKLQRLWILDSİGDKGLEVVASTCKELQELRVFPSDLLGG---GNTA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 VSHRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLD--HEEKITDL 431
65
                                                                                                                                                                                  LKLKGKPRAAMFNLI PEDWGGHVTPWVKEI SQYFDCLKSLHFRRMI VKDSDLQNLARDRG
                                                                                                                                                                                                                                                                             PLDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLE
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DEVIEHVFDFVTSHKDRNAISLVCKSWYKIERYSRQKVFIGNCYAINPERLLRRFFPCLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 VLNGCKKWKKLEIRDSP-FGDTALLADVSKYETMRSLWMSSCEVTLSGCKRLAEKAPWLN
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Liu S.K., Sakano H., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,
Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,
Vaysberg M., Altafi H., Brooks S., Buehler E., Chao O., Conn L.,
Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC FilX23 from Arabidopsis thaliana chromosome 1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.,
Submitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.
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idicots; rosids;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
01-007-2003 (TREMBLRel. 25, Last annotation update)
13.023.7 protein (Transport inhibitor response 1, putative).
13.023.7 protein (Transport inhibitor response 1, putative).
13.023.7 OR ATIG12820.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheopisperatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                             269 PERYSAISLPA--KLCRLGLTYIGKNELPIVFMFAAV--
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SEQUENCE FROM N.A.
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"Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                   N-FKSLVLVSCEGFTTDGLASIAANCRHLRELDLQENEIDDHRGQWLNCFPDSCTTLMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                  185 NFACLKGETNVAA-----LERLVARSPNLKSLKLNRAVPLDALARLMSCAPQLVDLGVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNEEPERYSAISLPAKLCRL-----GLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 YENEPDPESFAKLMTAIKKYTSLRSLSGFLEVAPLCLPAFYPICONLISLNLSYAAEIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHCM-LIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 VGLVAISAGCPKLHSILYFCKQMTNAALIAVAKNCPNFIRFRLCILEPHKPDHITFQSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEFAK
                     Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheng M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (Nov-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC092541; AAF78481.; -.
                                                                                                                                                                                                                                                               DVVLDCVIPYIDDPKDRDAVSQVCRRWYBLDSLTRKHVTIALCYTTTPARLRRRFPHLES
                                                                                                                                                                                                                                                                              HVLHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETL
                                                                                                                                                                                                                                                                                                                                                                                                         210 NFYL----TDIAVVKIEDLELLAKNCPNLVSVKLTDCEILD-LVNFFKHASALEEFCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLIALSOGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLD-HE-EKITDLPLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 GCKKMRKLEIRDSP-FGNAALLADVGRYETMRSLWMSSCEVTLGGCKRLAQNSPRLNVEI
                                                                                                                                                                                                                                         Gaps
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last amotation update)
11-Tunaport inhibitor response 1 protein (AT5949980/K9P8_12).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                 DB 10; Length 577;
                                                                                                                                                                                                              23.6%; Score 749.5; DB 10; Length 33.8%; Pred. No. 3.4e-55; ive 97; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | | | | | | | INENENNGMEQNEEDEREKVD---KLYLYRTVVGTRKDAPPYV 574
                                                                                                                                                                           Pfam; PF00646; F-box; 1. SEQUENCE 577 AA; 64906 MW; 8E419B4DB3068661 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 AA
                                                                                                                                               Interpro; IPR001810; F-box.
Interpro; IPR008945; Skpl_Skp2.
                                                                                                                               EMBL; BT002118; AAN72129.1; -.
                                                                                                                                                                                                                                      Matches 197; Conservative
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                                                                                                                                          PIR; F86261; F86261.
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1D 29LTX2
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DT 01-OC
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                       eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chan C.H., Dale U.M., Haysahizaki Y., Hauan V.W.,
Lishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Sarcou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
"Arabidopals ORF Clones.",
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  STRAIN=COlumbia;
MEDLINB=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C., Wu
                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty P1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Pall C.J., Quach H.L., Sakurai T., Sarou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., W. Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis cDNA clones."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Arabidopsis cDNA clones.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 619 AA; 69316 MW; D0614AF071EE4FD2 CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY056431; AAL08287.1; -. EMBL; AX139774; AAM98092.1; -. EMBL; BT004536; AAO42782.1; -.
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241

301

358 436

418 496 475 556 534

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319 HCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVSHRG 378
          YLTDIAVVKIE----DLELLAKNCPNLVSVKLTDCEILD-LVNFFKHASALEEFCGGTYN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Saxena S., Sievertzon M., Lundeborg J., Sandberg G., Bhalerao R.P.;
"The role of TIR1 related gene from hybrid aspen in regulating cambial
                                       242 DDFQTESYFKLTSALEKCKMLRSLSGFWDASPVCLSFIYPLCAQLTGLNLSYAPTLDASD
                                                                                                                                                                                                                                                                                                              379 LIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLLD--HEEKITDLPLDNG
                                                                                                                                                                                                                                       302 LIKMISRCVKLORLWVLDCISDKGLOVVASSCKOLOELRVFPSD---FYVAGYSAVTEEG
                                                                                                                                                                                                                                                                                                                                           476 KNIRKLEIRDSP-FGDAALLGNFARYETMRSLWMSSCNVTLKGCQVLASKMPMLNVEVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSLOKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 QVLENVLENVLENVLWFLTSRKDRNAASLVCRSWYRVEALTRSDLFIGNCYAVSPKRAMSRFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 LESLKLKGKPRAAMFNLIPEDWGGHVTPWVKEISQYFDCLKSLHFRRMIVKDSDLQNLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 N------EEPERYSAISLPAKL-CRLGLTYIGKNELPIVFMFAAVLKKLDLLYAMLD
                                                                                                                                                                                                                                                                                                                                                                                                            437 VRALLRGCDKLRRFALYLRRGGLTDVGLGYIGOYSPNVRWMLLGYVGESDAGLLEFAKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 FGAIVRECKGLORLSI----SGLLTDKVFMYIGKYAKQLEMLSIAFAGDSDKGMMHVMNGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 RVVDVVLDCVIPYIDDPKDRDAVSQVCRRWYELDSLTRKHVTIALCYTTTPARLRRRFPH
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Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I, Malpjahiales; Salicaceae; Saliceae, Populus.
NCBI_TaxID=47664;
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33.0%; Pred. No. 1.3e-52;
ive 94; Mismatches 260; Indels
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SEQUENCE 635 AA; 71202 MW; A2CDE4D9136B306B
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A July SEQUENCE FROM N.A.

A July S. Y., Ren S. X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F.,

A July J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,

RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,

RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng O.,

RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Lu Y.E., Mu Y.S., Wu Z.,

RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu Z.,

RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

Ajan Y.M., Xing W., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,

RA Shang R.Q., Guan J.P., Hong G.F.,

R. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ALGO6621, CAD40545.1;

DR EMBL, ALGO6621, CAD40545.1;

SQ SEQUENCE 575 AA; 64054 MW; 63EBFB6BSIOAF668 CRC64;
GLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLL-----DHEEKITDLP 432
                                                                                                                                                                                                                                                                                                                                   465
                                                                                                                                                                                                                                                                                                                                                                               LDNGVRALLRGCDKLRRFALYLRRGGLTDVGLGYIGQYSPNVRWMLLGYVGESDAGLLEF 492
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                                                                         -NEEPER----YSAISLPAK--LCRLGLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTE
                                                                                                                           HDEEPQSEQEPDYAAAFRACKSVVCLSGFRELMPEYLPAIFPVCANLTSLNFSYANISPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKGCPSLOKLEMRGCLFFSERALAVAATQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 LHALKLDKCSGFTTDGLFHIGRFCKSLRVLFLEESSILEKDGEWLHELALNNTVLETLNF
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 EVIGSDDDDNRDYVETLYM-----YRSLDGPRNDAPKFVTIL 619
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Last annotation update)
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                                      WVKEISQYFDCLKSLHFRRMIVKDSDLQNLARDRGHVLHALKLDKCSGFTTDGLFHIGRF 174
SWYRVEAQTRLEVFIGNCYSLSPARLIHRFKRVRSLVLKGKPRFADFNLMPPNWGAQFSP 131
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                                                                                                                                    370 AVAATCKELRELRIFPFDP---REDSEGPVSGVGLQAISEGCRKLESILYFCQNMTNGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 HRYSNMRFVWLSSCLISRGGCRGVSHALPNVVVEVFG----ADGDDDEDTVTGDYVETLY
                                                                        WVAATAKAYPWLEKVHLKRMFVTDDDLALLA-ESFPGFKELTLVCCEGFGTSGIAIVANK
                                                                                                              CKSLRVLFLEESSILEKDGEWLHELALNNTVLETINFYLTDIAVVKIEDLELLAKNCPNL
                                                                                                                                                                                           235 VSVKLTD-CEILDLVNFFKHASALEEFCGGTYN-----EEPERYSAISLPAK--LCRL
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
AT4924390/T22A6 220.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
euroaids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis cDNA clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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SPSEDVSQVEQOPDYASAFAACKSLVCLSGFREIIPDYLFAINPVCANLTSLNFSFADVS 365
                                                            316 TEDHCMLIQRCPNLEVLETRNVIGDRGLEVLGRCCKRLKRLRIERGDDDQGMEDEEGTVS 375
                                                                                                                                      --DHEEKITD 430
                                                                                                                                                                                                                                                   480 EPMDEGFGAIVKNCKKLTRLAV---SGLLTDRAFAYIGKYGKIVRTLSVAFAGDSDMGLK 536
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                                                                                  366 AEQLKPIISNCHKLQIFWVLDSICDEGLQAVAATCKELRELRVFPVDP---REDIEGFVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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21.8*; Score 693; DB 10; Length 61.
Best Local Similarity 30.7*; Pred. No. 2.5e-50;
Matches 190; Conservative 108; Mismatches 277; Indels
                                                                                                                                      376 HRGLIALSQGCSELEYMAVYVSDITNASLEHIGTHLKNLCDFRLVLL--
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALOY8637; CAB45074.1; -.
EMBL; ALO16561; CAB79349.1; -.
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                              551 NIELIPSRKVATNTNPDETVVVEHPAHILAYYSLAGQRSDFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport inhibitor response-like protein. 1722A6.220 OR AT4G24390.
Arabidopsis thaliana (Mouse-ear cress).
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InterPro; IPR001810; F-box.
Pfam; PF00646; F-box; 1.
SEQUENCE 614 AA; 68520 MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 EHIGTHLKNLCDFRLVLL----DHEEKITDLPLDNGVRALLRGCDKLRRFALYLRRGGL 459
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                                                                                                                                                                                                                                                                                                                                                                                                                     235 VSVKLTD-CEILDLVNFFKHASALBEFCGGTYN-----BEPERYSAISLPAK--LCRL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLTYIGKNELPIVFMFAAVLKKLDLLYAMLDTEDHCMLIQRCPNLEVLETRNVIGDRGLE 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQLTSLRYLWVQGYGVSPSGRDLLVMARPFWNIELIPSRKVATNTNPDETVVVEHPAHIL
                                                                                                       Query Match 21.8%; Score 693; DB 10; Length 623; Best Local Similarity 30.7%; Pred. No. 2.6e-50; Matches 190; Conservative 108; Mismatches 277; Indels 4.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY091772; AAM10320.1; -.
EMBL; BT006340; AAP21148.1; -.
InterPro: IPROMOTO: Phox.
Pfam; PF00046; F-box. 1.
SEQUENCE 623 AA; 69499 MW; 7007CD6F4F5B2C9C CRC64;
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